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- <110> Genentech, Inc.  
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Williams, P. Mickey  
Wood, William, I.
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- <150> US 60/145,698  
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- <150> US 60/146,222  
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Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr  
 35 40 45

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr  
 50 55 60

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu  
 65 70 75 80

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala  
 85 90 95

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr  
 100 105 110

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys  
 115 120 125

Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser  
 130 135 140

0905348.0.1301

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg  
 145 150 155 160  
 Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
 165 170 175  
 Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
 180 185 190  
 His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
 195 200 205  
 Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
 210 215 220  
 Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
 225 230 235 240  
 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
 245 250 255  
 Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
 260 265 270  
 Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
 275 280 285  
 Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
 290 295 300  
 Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro  
 305 310 315 320  
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 aacagccctg gctgagggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180  
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090548-01100

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<211> 379
<212> PRT
<213> Homo sapiens
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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu  
35 40 45  
Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala  
50 55 60  
Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

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				85					90					95	
Ala	Glu	Tyr	Phe	Tyr	Glu	Phe	Leu	Ser	Leu	Arg	Ser	Leu	Asp	Lys	Gly
			100					105					110		
Ile	Met	Ala	Asp	Pro	Thr	Val	Asn	Val	Pro	Leu	Leu	Gly	Thr	Val	Pro
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His	Lys	Ala	Ser	Val	Val	Gln	Val	Gly	Phe	Pro	Cys	Leu	Gly	Lys	Gln
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Asp	Gly	Val	Ala	Ala	Phe	Glu	Val	Asp	Val	Ile	Val	Met	Asn	Ser	Glu
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Gly	Asn	Thr	Ile	Leu	Gln	Thr	Pro	Gln	Asn	Ala	Ile	Phe	Phe	Lys	Thr
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Asn	Glu	Arg	Arg	Ile	Cys	Glu	Cys	Pro	Asp	Gly	Phe	His	Gly	Pro	His
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				245					250					255	
Phe	Tyr	Pro	Gly	Lys	Cys	Ile	Cys	Pro	Pro	Gly	Leu	Glu	Gly	Glu	Gln
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Cys	Ser	Lys	Pro	Val	Cys	Glu	Pro	Gly	Cys	Gly	Ala	His	Gly	Thr	Cys
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His	Glu	Pro	Asn	Lys	Cys	Gln	Cys	Gln	Glu	Gly	Trp	His	Gly	Arg	His
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FOEF20-BHE50650

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu  
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<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
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21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
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22

<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
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49

0905348-071301  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 9  
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<210> 10  
 <211> 23  
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<210> 11  
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Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
    35             40             45

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
    50             55             60

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
    65             70             75             80

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
    85             90             95

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
   100             105             110

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
   115             120             125

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
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Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
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His Asp Pro Gly

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F02T2208HE0660

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 <223> a, t, c or g

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 <223> a, t, c or g

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 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

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 oligonucleotide probe

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09905348.01301

ttcgaggcct ctgagaagtg gccc

24

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 15

ggcggatatct ctctggcctc cc

22

<210> 16

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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50

<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

<400> 17

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<210> 18

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<212> PRT

<213> Homo sapiens

TOGETHER

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Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp  
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala  
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln  
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<223> Description of Artificial Sequence: Synthetic  
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&lt;400&gt; 19

tgctgtgcta ctcctgcaaa gccc

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F00120-24E50650

<213> Artificial Sequence

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oligonucleotide probe

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24

<210> 21

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<212> DNA

<213> Artificial Sequence

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oligonucleotide probe

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agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

TOCT-20-2450660

&lt;400&gt; 23

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu  
 1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
 195 200 205

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

&lt;210&gt; 25

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gccca 24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
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<210> 27  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
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<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

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  1                               5                10                15

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
                20                25                30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
                35                40                45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
  50                55                60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
  65                70                75                80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
                85                90                95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
                100                105                110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
                115                120                125

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09905348.0.1301



Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
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 145 150 155 160  
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175  
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190  
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205  
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220  
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240  
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255  
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270  
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
 275 280 285  
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
 290 295 300  
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
 305 310 315 320  
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
 325 330 335  
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350  
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro  
 355 360 365  
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

0905348-01301

405 410 415  
 Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val  
 420 425 430  
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 435 440 445  
 Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly  
 450 455 460  
 Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu  
 465 470 475 480  
 Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu  
 485 490 495  
 Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala  
 500 505 510  
 Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser  
 515 520 525  
 His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala  
 530 535 540  
 Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser  
 545 550 555 560  
 Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys  
 565 570 575  
 Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly  
 580 585 590  
 Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln  
 595 600 605  
 Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu  
 610 615 620  
 Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His  
 625 630 635 640  
 Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu  
 645 650 655  
 His Cys His Thr  
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<210> 29  
 <211> 21  
 <212> DNA

TEET 20" 34E50650

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29

cggtctacct gtatggcaac c 21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac 22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc 22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac 46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

acttgagca agcggcggcg gcggagacag aggcagaggc agaagctggg gctccgtcct 60  
cgctccccc gagcgatccc cgaggagagc cgcggccctc ggcgaggcga agaggccgac 120

TEF20"84E50650

**Abstract**

ctgtagaaca ctggccatag gaaatgctgt ttttttgtac tggactttac cttgatatat 3360  
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 ttatacaata ttaaaattca ccacttcag 3449

<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile  
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Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile  
 20 25 30

Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu  
 35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser  
 50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile  
 65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val  
 85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys  
 100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg  
 115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu  
 130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn  
 145 150 155 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser  
 165 170 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe  
 180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly  
 195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln  
 210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

09905348.071301

225		230		235		240
Met Cys Ser Thr	Leu Glu His Asn Cys	Ala His Phe Cys	Ile Asn Ile			
	245	250	255			
Pro Gly Ser Tyr	Val Cys Arg Cys	Lys Gln Gly Tyr	Ile Leu Asn Ser			
	260	265	270			
Asp Gln Thr Thr	Cys Arg Ile Gln Asp	Leu Cys Ala Met	Glu Asp His			
	275	280	285			
Asn Cys Glu Gln	Leu Cys Val Asn Val	Pro Gly Ser Phe	Val Cys Gln			
	290	295	300			
Cys Tyr Ser Gly	Tyr Ala Leu Ala	Glu Asp Gly Lys	Arg Cys Val Ala			
305	310	315	320			
Val Asp Tyr Cys	Ala Ser Glu Asn His	Gly Cys Glu His	Glu Cys Val			
	325	330	335			
Asn Ala Asp Gly	Ser Tyr Leu Cys	Gln Cys His Glu	Gly Phe Ala Leu			
	340	345	350			
Asn Pro Asp Glu	Lys Thr Cys Thr	Arg Ile Asn Tyr	Cys Ala Leu Asn			
	355	360	365			
Lys Pro Gly Cys	Glu His Glu Cys	Val Asn Met Glu	Glu Ser Tyr Tyr			
	370	375	380			
Cys Arg Cys His	Arg Gly Tyr Thr	Leu Asp Pro Asn	Gly Lys Thr Cys			
385	390	395	400			
Ser Arg Val Asp	His Cys Ala Gln	Gln Asp His Gly	Cys Glu Gln Leu			
	405	410	415			
Cys Leu Asn Thr	Glu Asp Ser Phe	Val Cys Gln Cys	Ser Glu Gly Phe			
	420	425	430			
Leu Ile Asn Glu	Asp Leu Lys Thr	Cys Ser Arg Val	Asp Tyr Cys Leu			
	435	440	445			
Leu Ser Asp His	Gly Cys Glu Tyr	Ser Cys Val Asn	Met Asp Arg Ser			
	450	455	460			
Phe Ala Cys Gln	Cys Pro Glu Gly	His Val Leu Arg	Ser Asp Gly Lys			
465	470	475	480			
Thr Cys Ala Lys	Leu Asp Ser Cys	Ala Leu Gly Asp	His Gly Cys Glu			
	485	490	495			
His Ser Cys Val	Ser Ser Glu Asp	Ser Phe Val Cys	Gln Cys Phe Glu			
	500	505	510			

05905348-071001  
F01E720-84E50660

Gly	Tyr	Ile	Leu	Arg	Glu	Asp	Gly	Lys	Thr	Cys	Arg	Arg	Lys	Asp	Val
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Cys	Gln	Ala	Ile	Asp	His	Gly	Cys	Glu	His	Ile	Cys	Val	Asn	Ser	Asp
		530				535				540					
Asp	Ser	Tyr	Thr	Cys	Glu	Cys	Leu	Glu	Gly	Phe	Arg	Leu	Ala	Glu	Asp
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Gly	Lys	Arg	Cys	Arg	Arg	Lys	Asp	Val	Cys	Lys	Ser	Thr	His	His	Gly
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Cys	Glu	His	Ile	Cys	Val	Asn	Asn	Gly	Asn	Ser	Tyr	Ile	Cys	Lys	Cys
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Ser	Glu	Gly	Phe	Val	Leu	Ala	Glu	Asp	Gly	Arg	Arg	Cys	Lys	Lys	Cys
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Leu	Gly	Glu	Glu	Asn	Phe	Glu	Val	Val	Lys	Gln	Phe	Val	Thr	Gly	Ile
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Ile	Asp	Ser	Leu	Thr	Ile	Ser	Pro	Lys	Ala	Ala	Arg	Val	Gly	Leu	Leu
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Gln	Tyr	Ser	Thr	Gln	Val	His	Thr	Glu	Phe	Thr	Leu	Arg	Asn	Phe	Asn
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Ser	Ala	Lys	Asp	Met	Lys	Lys	Ala	Val	Ala	His	Met	Lys	Tyr	Met	Gly
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Phe	Thr	Gln	Gly	Glu	Gly	Ala	Arg	Pro	Leu	Ser	Thr	Arg	Val	Pro	Arg
		705		710						715				720	
Ala	Ala	Ile	Val	Phe	Thr	Asp	Gly	Arg	Ala	Gln	Asp	Asp	Val	Ser	Glu
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Trp	Ala	Ser	Lys	Ala	Lys	Ala	Asn	Gly	Ile	Thr	Met	Tyr	Ala	Val	Gly
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Val	Gly	Lys	Ala	Ile	Glu	Glu	Glu	Leu	Gln	Glu	Ile	Ala	Ser	Glu	Pro
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Thr	Asn	Lys	His	Leu	Phe	Tyr	Ala	Glu	Asp	Phe	Ser	Thr	Met	Asp	Glu
		770				775				780					
Ile	Ser	Glu	Lys	Leu	Lys	Lys	Gly	Ile	Cys	Glu	Ala	Leu	Glu	Asp	Ser
		785		790						795				800	

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
850 855 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
865 870 875 880

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln  
885 890 895

Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu  
900 905 910

Arg Tyr Arg  
915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 35

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 36

acagccatgg tctatagctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

TOPFLO" 84E5D66D



&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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45

&lt;210&gt; 38

&lt;211&gt; 1813

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

```

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1813

```

&lt;210&gt; 39

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

T00120-3450550

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Phe	Leu	Gly	Leu	Ser	Ala	Leu	Ala	Pro	Pro	Ser	Arg	Ala	Gln	Leu	Gln				
			20					25					30						
Leu	His	Leu	Pro	Ala	Asn	Arg	Leu	Gln	Ala	Val	Glu	Gly	Gly	Glu	Val				
		35					40					45							
Val	Leu	Pro	Ala	Trp	Tyr	Thr	Leu	His	Gly	Glu	Val	Ser	Ser	Ser	Gln				
	50					55					60								
Pro	Trp	Glu	Val	Pro	Phe	Val	Met	Trp	Phe	Phe	Lys	Gln	Lys	Glu	Lys				
65					70					75					80				
Glu	Asp	Gln	Val	Leu	Ser	Tyr	Ile	Asn	Gly	Val	Thr	Thr	Ser	Lys	Pro				
				85					90					95					
Gly	Val	Ser	Leu	Val	Tyr	Ser	Met	Pro	Ser	Arg	Asn	Leu	Ser	Leu	Arg				
			100					105					110						
Leu	Glu	Gly	Leu	Gln	Glu	Lys	Asp	Ser	Gly	Pro	Tyr	Ser	Cys	Ser	Val				
		115					120					125							
Asn	Val	Gln	Asp	Lys	Gln	Gly	Lys	Ser	Arg	Gly	His	Ser	Ile	Lys	Thr				
	130					135					140								
Leu	Glu	Leu	Asn	Val	Leu	Val	Pro	Pro	Ala	Pro	Pro	Ser	Cys	Arg	Leu				
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Gln	Gly	Val	Pro	His	Val	Gly	Ala	Asn	Val	Thr	Leu	Ser	Cys	Gln	Ser				
				165					170					175					
Pro	Arg	Ser	Lys	Pro	Ala	Val	Gln	Tyr	Gln	Trp	Asp	Arg	Gln	Leu	Pro				
			180					185					190						
Ser	Phe	Gln	Thr	Phe	Phe	Ala	Pro	Ala	Leu	Asp	Val	Ile	Arg	Gly	Ser				
	195						200					205							
Leu	Ser	Leu	Thr	Asn	Leu	Ser	Ser	Ser	Met	Ala	Gly	Val	Tyr	Val	Cys				
	210					215					220								
Lys	Ala	His	Asn	Glu	Val	Gly	Thr	Ala	Gln	Cys	Asn	Val	Thr	Leu	Glu				
225					230					235					240				
Val	Ser	Thr	Gly	Pro	Gly	Ala	Ala	Val	Val	Ala	Gly	Ala	Val	Val	Gly				
				245					250					255					
Thr	Leu	Val	Gly	Leu	Gly	Leu	Leu	Ala	Gly	Leu	Val	Leu	Leu	Tyr	His				
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Arg	Arg	Gly	Lys	Ala	Leu	Glu	Glu	Pro	Ala	Asn	Asp	Ile	Lys	Glu	Asp				
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FOET 20 " 9450650

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 42  
 ggccacagca tcaaaacctt agaactcaat gtactgggtc ctccagctcc 50  
  
 <210> 43  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 43  
 gtgtgacaca gcgtgggc 18  
  
 <210> 44  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 44  
 gaccggcagg cttctgcg 18  
  
 <210> 45  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 45  
 cagcagcttc agccaccagg agtgg 25  
  
 <210> 46  
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 <212> DNA  
 <213> Artificial Sequence  
  
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 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe  
  
 <400> 46  
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 <210> 47

<211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 47

ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc

45

<210> 48

<211> 2822

<212> DNA

<213> Homo sapiens

<400> 48

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 gtgaaatacg caatggaatt gaagcctgct attgcaacat gggattttca ggaaatgggtg 180  
 tcacaatttg tgaagatgat aatgaatgtg gaaatttaac tcagtcctgt ggcgaaaatg 240  
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 gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360  
 caaactgcc tttagataat gtctgtatag ctgcaaata taataaaact ttaacaaaaa 420  
 tcagatccat aaaagaacct gtggcctttgc tacaagaagt ctatagaaat tctgtgacag 480  
 atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540  
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090548 034E50660

```

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aa
2822

```

<210> 49  
 <211> 690  
 <212> PRT  
 <213> Homo sapiens

<400> 49

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Met Lys Arg Leu Pro Leu Leu Val Val Phe Ser Thr Leu Leu Asn Cys
  1              5              10              15

```

```

Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
      20              25              30

```

```

Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
      35              40              45

```

```

Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
      50              55              60

```

```

Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
      65              70              75              80

```

```

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
      85              90              95

```

```

Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
      100             105             110

```

```

Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
      115             120             125

```

```

Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
      130             135             140

```

```

Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
      145             150             155             160

```

```

Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
      165             170             175

```

```

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

```

090546-071301

	180		185		190
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val	195	200	205		
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys	210	215	220		
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe	225	230	235	240	
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys	245	250	255		
Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met	260	265	270		
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala	275	280	285		
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser	290	295	300		
Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln	305	310	315	320	
Asn Tyr Asp Asn Ser Glu Glu Glu Glu Arg Val Ile Ser Ser Val Ile	325	330	335		
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys	340	345	350		
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser	355	360	365		
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp	370	375	380		
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser	385	390	395	400	
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly	405	410	415		
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln	420	425	430		
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr	435	440	445		
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys	450	455	460		

TOEFL-0-84E50660

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<210> 50
<211> 589
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (61)
```



<223> a, t, c or g

<400> 50

```

tggaacata tcctccctca tatgaatatg gatggagact acataaatat atttccaaag 60
ngaaaagccg gcatatggat tcaaattggca atgttgcagt tgcattttta tattataaga 120
gtattggtcc ctttgctttc atcatctgac aacttcttat tgaaacctca aaattatgat 180
aattctgaag aggaggaaag agtcatatct tcagtaattt cagtctcaat gagctcaaac 240
ccaccacat tatatgaact tgaaaaaata acatttacat taagtcacgc aaaggtcaca 300
gataggtata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
tggtcttcag agggctgtga gctgacatac tcaaattgaga cccacacctc atgcccgtgt 420
aatcacctga cacattttgc aattttgatg tcctctgggc cttccattgg tattaagat 480
tataatatcc ttacaaggat cactcaacta ggaataatta tttcactgat ttgtcttgcc 540
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

```

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 51

ggtaatgagc tccattacag 20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg 18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag 22

<210> 54

<211> 18

<212> DNA

TOFT-0-84E0660

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 55

ggatctcctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 57

atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaaccgggc 60  
cgctaagcga ggctcctcc tcccgcagat ccgaacggcc tgggcgggggt caccocggct 120

TTCTTCTG"84E50650

```

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cgggccggag ccgcgcgcgc gtcagagcag gagcgctgcg tccaggatct agggccacga 360
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gaaccctttc ccagcactt ggttttccaa catgatatt atgagtaatt tattttgata 2040
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```

&lt;210&gt; 59

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 59

```

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
  1                      5                      10                      15

```

```

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
                20                      25                      30

```

```

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
    35                      40                      45

```

```

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
    50                      55                      60

```

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
 65 70 75 80  
 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
 85 90 95  
 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
 100 105 110  
 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
 115 120 125  
 Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
 130 135 140  
 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
 145 150 155 160  
 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
 165 170 175  
 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
 180 185 190  
 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
 195 200 205  
 Val Arg Ser Pro Ser Phe Glu Lys  
 210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 60

atccgcccag atggctacaa tgtgta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 61

gcctcccggg ctccctgagc agtgccaaac agcggcagtg ta

42

090548-071341

<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtcgggt gacaagccca aa

22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
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 gctgctgctg cgctacctgg tggcgccct gggtatcat aaggcctatg gggtttctgc 180  
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggcctatt tagcctgcaa 240  
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 ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360  
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 tggcatccgt ttgctagaaa atcccagact tggctcccaa agcaccaaca gctcatacac 660  
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 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
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 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
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 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
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 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
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 Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
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305 310

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 <212> DNA  
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<210> 66  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 66  
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<210> 67  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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 <212> DNA  
 <213> Homo sapiens

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 actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480  
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&lt;210&gt; 69

&lt;211&gt; 708

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 69

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Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
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Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
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Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
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Lys	Lys	Met 115	Pro	Gln	Leu	Leu	Ser	Val	Tyr	Leu	Glu	Glu	Asn	Lys	Leu
Thr	Glu 130	Leu	Pro	Glu	Lys	Cys 135	Leu	Ser	Glu	Leu	Ser 140	Asn	Leu	Gln	Glu
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Gln	Lys	Val	Val 260	Asn	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	Asn	Pro	Ile
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Val 305	Asp	Asn	Leu	Pro	Asp 310	Leu	Arg	Lys	Ile	Glu 315	Ala	Thr	Asn	Asn	Pro 320
Arg	Leu	Ser	Tyr 325	Ile	His	Pro	Asn	Ala	Phe 330	Phe	Arg	Leu	Pro	Lys	Leu 335
Glu	Ser	Leu	Met	Leu	Asn	Ser	Asn	Ala	Leu	Ser	Ala	Leu	Tyr	His	Gly

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Pro	Ile	Arg	Cys	Asp	Cys	Val	Ile	Arg	Trp	Met	Asn	Met	Asn	Lys	Thr
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Val	Asp	Gly	Ser	Phe	Pro	Gln	Asp	Asn	Asn	Gly	Ser	Leu	Asn	Ile	Lys
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Ile	Arg	Asp	Ile	Gln	Ala	Asn	Ser	Val	Leu	Val	Ser	Trp	Lys	Ala	Ser
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Val	Tyr	Asn	Leu	Thr	His	Leu	Asn	Pro	Ser	Thr	Glu	Tyr	Lys	Ile	Cys
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Ile	Asp	Ile	Pro	Thr	Ile	Tyr	Gln	Lys	Asn	Arg	Lys	Lys	Cys	Val	Asn
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Val	Thr	Thr	Lys	Gly	Leu	His	Pro	Asp	Gln	Lys	Glu	Tyr	Glu	Lys	Asn
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Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
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Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
705

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<212> DNA  
<213> Homo sapiens

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<210> 71  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 71

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 35 40 45  
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro  
 50 55 60  
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro  
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 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser  
 85 90 95  
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala  
 100 105 110  
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val  
 115 120 125  
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn  
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 165 170 175  
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 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr  
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 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys  
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&lt;210&gt; 72

&lt;211&gt; 2290

FOOTNOTES: 07450660

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

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aaaaaaaaaa 2290

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&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

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 Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala  
 50 55 60  
 Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys  
 65 70 75 80  
 Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His  
 85 90 95  
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 180 185 190  
 Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr  
 195 200 205  
 Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His  
 210 215 220  
 Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg  
 225 230 235 240  
 Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr  
 245 250 255  
 Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His  
 260 265 270  
 Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr  
 275 280 285  
 Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly  
 290 295 300

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Ser	Met	Leu	His	Glu	Leu	Leu	Arg	Leu	Gln	Glu	Ile	Gln	Leu	Val	Gly	
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Gly	Gln	Leu	Ala	Val	Val	Glu	Pro	Tyr	Ala	Phe	Arg	Gly	Leu	Asn	Tyr	
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Leu	Arg	Val	Leu	Asn	Val	Ser	Gly	Asn	Gln	Leu	Thr	Thr	Leu	Glu	Glu	
340					345					350						
Ser	Val	Phe	His	Ser	Val	Gly	Asn	Leu	Glu	Thr	Leu	Ile	Leu	Asp	Ser	
355					360					365						
Asn	Pro	Leu	Ala	Cys	Asp	Cys	Arg	Leu	Leu	Trp	Val	Phe	Arg	Arg	Arg	
370					375					380						
Trp	Arg	Leu	Asn	Phe	Asn	Arg	Gln	Gln	Pro	Thr	Cys	Ala	Thr	Pro	Glu	
385					390					395					400	
Phe	Val	Gln	Gly	Lys	Glu	Phe	Lys	Asp	Phe	Pro	Asp	Val	Leu	Leu	Pro	
405					410					415						
Asn	Tyr	Phe	Thr	Cys	Arg	Arg	Ala	Arg	Ile	Arg	Asp	Arg	Lys	Ala	Gln	
420					425					430						
Gln	Val	Phe	Val	Asp	Glu	Gly	His	Thr	Val	Gln	Phe	Val	Cys	Arg	Ala	
435					440					445						
Asp	Gly	Asp	Pro	Pro	Pro	Ala	Ile	Leu	Trp	Leu	Ser	Pro	Arg	Lys	His	
450					455					460						
Leu	Val	Ser	Ala	Lys	Ser	Asn	Gly	Arg	Leu	Thr	Val	Phe	Pro	Asp	Gly	
465					470					475					480	
Thr	Leu	Glu	Val	Arg	Tyr	Ala	Gln	Val	Gln	Asp	Asn	Gly	Thr	Tyr	Leu	
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Cys	Ile	Ala	Ala	Asn	Ala	Gly	Gly	Asn	Asp	Ser	Met	Pro	Ala	His	Leu	
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His	Val	Arg	Ser	Tyr	Ser	Pro	Asp	Trp	Pro	His	Gln	Pro	Asn	Lys	Thr	
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Phe	Ala	Phe	Ile	Ser	Asn	Gln	Pro	Gly	Glu	Gly	Glu	Ala	Asn	Ser	Thr	
530					535					540						
Arg	Ala	Thr	Val	Pro	Phe	Pro	Phe	Asp	Ile	Lys	Thr	Leu	Ile	Ile	Ala	
545					550					555					560	
Thr	Thr	Met	Gly	Phe	Ile	Ser	Phe	Leu	Gly	Val	Val	Leu	Phe	Cys	Leu	
565					570					575						
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580	585	590	
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<210> 75			
<211> 23			
<212> DNA			
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<400> 75			
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<210> 76			
<211> 52			
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<213> Artificial Sequence			
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gg			52
<210> 77			
<211> 22			
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<213> Artificial Sequence			
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24

<211> 50  
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 <213> Artificial Sequence

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<210> 83  
 <211> 1685  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
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 agccagggag ccggccggga agcgcgatgg gggccccagc cgctcgctc ctgctcctgc 180  
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 tgaaagatca cgaggactca tcctgcaat ggtctaacct tgcacagcag actctctact 360  
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 ccctttccgt ggcttctctg catttggggt attattattt ttgtaacaat cccaaatcaa 1620  
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 aaaca 1685

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 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

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 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu  
 35 40 45  
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn  
 50 55 60  
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp  
 65 70 75 80  
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 85 90 95  
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile  
 100 105 110  
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly  
 115 120 125  
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 130 135 140  
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala  
 145 150 155 160  
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro  
 165 170 175  
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser  
 180 185 190  
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val  
 195 200 205  
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser  
 210 215 220  
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp  
 225 230 235 240  
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly  
 245 250 255  
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser  
 260 265 270  
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe  
 275 280 285

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Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn  
 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser  
 305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile  
 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly  
 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys  
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Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile  
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<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

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## oligonucleotide probe

&lt;400&gt; 87

cctagcacag tgacgaggga cttggc

26

&lt;210&gt; 88

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 88

aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc

50

&lt;210&gt; 89

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 89

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&lt;210&gt; 90

&lt;211&gt; 2755

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 90

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F00740-84E0660

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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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      20             25             30

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Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
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```

```

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
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```

```

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
    65             70             75             80

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```

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
      85             90             95

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Ile	Asp	Pro	Gly	Ala	Phe	Gln	Asp	Leu	Asn	Lys	Leu	Glu	Val	Leu	Ile
Leu	Asn	Asp	Asn	Leu	Ile	Ser	Thr	Leu	Pro	Ala	Asn	Val	Phe	Gln	Tyr
Val	Pro	Ile	Thr	His	Leu	Asp	Leu	Arg	Gly	Asn	Arg	Leu	Lys	Thr	Leu
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Pro	Phe	Lys	Thr	Asn	Gly	Gln	Glu	Asp	His	Ala	Thr	Pro	Gly	Ser	Ala
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Pro	Thr	Ala	Ala	Ile	Ala	Thr	Gly	Ser	Ser	Arg	Asn	Lys	Pro	Leu	Ala
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Ser	Gly	Leu	Lys	Met	Asn	Cys	Asn	Asn	Arg	Asn	Val	Ser	Ser	Leu	Ala
Asp	Leu	Lys	Pro	Lys	Leu	Ser	Asn	Val	Gln	Glu	Leu	Phe	Leu	Arg	Asp

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 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn  
 465 470 475 480  
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu  
 485 490 495  
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala  
 500 505 510  
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly  
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 530 535 540  
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr  
 545 550 555 560  
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu  
 565 570 575  
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 580 585 590  
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser  
 595 600 605  
 Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu  
 610 615 620  
 Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val  
 625 630 635 640  
 Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser  
 645 650 655  
 Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr

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660 665 670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp  
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Cys Gly Ser His Ser Leu Ser Asp  
690 695

<210> 92  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 93  
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<212> DNA  
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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 94  
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<210> 95  
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<212> DNA  
<213> Homo sapiens

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TOE120"84E50660

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<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

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Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser  
 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60

TOEFL-20-24E50650

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
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 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110  
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
 115 120 125  
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140  
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160  
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175  
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
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 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
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 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220  
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240  
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
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 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270  
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
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 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
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 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
 305 310 315 320  
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09905348-04301

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 97
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<210> 98
<211> 20
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 98
tgaccagtgg ggaaggacag
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20

<210> 99  
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 <212> DNA  
 <213> Artificial Sequence  
  
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         oligonucleotide probe  
  
 <400> 101  
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 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 102  
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 <210> 103  
 <211> 2026  
 <212> DNA  
 <213> Homo sapiens

0905348-01301  
 T00120-B4E50660

&lt;400&gt; 103

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&lt;210&gt; 104

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

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Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
      20              25              30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
      35              40              45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
      50              55              60

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0905348.07301

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Glu	Ser	Asp	Asn	Leu	Cys	Arg	Tyr	Asp	Phe	Val	Asp	Val	Tyr	Asn	Gly	85	90	95	
His	Ala	Asn	Gly	Gln	Arg	Ile	Gly	Arg	Phe	Cys	Gly	Thr	Phe	Arg	Pro	100	105	110	
Gly	Ala	Leu	Val	Ser	Ser	Gly	Asn	Lys	Met	Met	Val	Gln	Met	Ile	Ser	115	120	125	
Asp	Ala	Asn	Thr	Ala	Gly	Asn	Gly	Phe	Met	Ala	Met	Phe	Ser	Ala	Ala	130	135	140	
Glu	Pro	Asn	Glu	Arg	Gly	Asp	Gln	Tyr	Cys	Gly	Gly	Leu	Leu	Asp	Arg	145	150	155	160
Pro	Ser	Gly	Ser	Phe	Lys	Thr	Pro	Asn	Trp	Pro	Asp	Arg	Asp	Tyr	Pro	165	170	175	
Ala	Gly	Val	Thr	Cys	Val	Trp	His	Ile	Val	Ala	Pro	Lys	Asn	Gln	Leu	180	185	190	
Ile	Glu	Leu	Lys	Phe	Glu	Lys	Phe	Asp	Val	Glu	Arg	Asp	Asn	Tyr	Cys	195	200	205	
Arg	Tyr	Asp	Tyr	Val	Ala	Val	Phe	Asn	Gly	Gly	Glu	Val	Asn	Asp	Ala	210	215	220	
Arg	Arg	Ile	Gly	Lys	Tyr	Cys	Gly	Asp	Ser	Pro	Pro	Ala	Pro	Ile	Val	225	230	235	240
Ser	Glu	Arg	Asn	Glu	Leu	Leu	Ile	Gln	Phe	Leu	Ser	Asp	Leu	Ser	Leu	245	250	255	
Thr	Ala	Asp	Gly	Phe	Ile	Gly	His	Tyr	Ile	Phe	Arg	Pro	Lys	Lys	Leu	260	265	270	
Pro	Thr	Thr	Thr	Glu	Gln	Pro	Val	Thr	Thr	Thr	Phe	Pro	Val	Thr	Thr	275	280	285	
Gly	Leu	Lys	Pro	Thr	Val	Ala	Leu	Cys	Gln	Gln	Lys	Cys	Arg	Arg	Thr	290	295	300	
Gly	Thr	Leu	Glu	Gly	Asn	Tyr	Cys	Ser	Ser	Asp	Phe	Val	Leu	Ala	Gly	305	310	315	320
Thr	Val	Ile	Thr	Thr	Ile	Thr	Arg	Asp	Gly	Ser	Leu	His	Ala	Thr	Val	325	330	335	
Ser	Ile	Ile	Asn	Ile	Tyr	Lys	Glu	Gly	Asn	Leu	Ala	Ile	Gln	Gln	Ala				

FOET-20-84E50660

340	345	350
Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro		
355	360	365
Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu		
370	375	380
Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys		
385	390	395
Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys		
405	410	415

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 105

ccgattcata gacctcgaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

<211> 1838

<212> DNA

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<213> Homo sapiens

<400> 108

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<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

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 20 25 30  
 Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr  
 35 40 45  
 Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile  
 50 55 60

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Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu  
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 Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly  
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 Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser  
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 Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro  
 115 120 125  
 Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro  
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 Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu  
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 Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys  
 180 185 190  
 Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His  
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 Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro  
 210 215 220  
 Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His  
 225 230 235 240  
 Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys  
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 Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg  
 260 265 270  
 Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg  
 275 280 285  
 Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu  
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 Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln  
 305 310 315 320  
 Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr  
 325 330 335  
 Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala  
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Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
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Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
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Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
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Ile Lys Gly Arg  
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<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
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<400> 110

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<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc 22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac 22

<210> 113

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 090548-0101

<211> 1616  
 <212> DNA  
 <213> Homo sapiens

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 <223> a, t, c or g

<400> 113  
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<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
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 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45

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Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu  
 50 55 60  
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 65 70 75 80  
 Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr  
 85 90 95  
 His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu  
 100 105 110  
 Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala  
 115 120 125  
 Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg  
 130 135 140  
 Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr  
 145 150 155 160  
 Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys  
 165 170 175  
 Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg  
 180 185 190  
 Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu  
 195 200 205  
 Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln  
 210 215 220  
 Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu  
 225 230 235 240  
 Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro  
 245 250 255  
 Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu  
 260 265 270  
 Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe  
 275 280 285  
 Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu  
 290 295 300  
 Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu  
 305 310 315 320  
 Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr  
 325 330 335

0905348-0130  
 TDE120-BHE50660

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<400> 118
gtctgttccc aggagtcctt cggcggtgtg tgtgtcagtg gcttgatcgc gatggggaca 60
aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgctcc 120
ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180
```

aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtgggaag 240  
tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300  
gaggaccggg tgaccttctt gccaaactgg atcaccttca agtccgtgac acgggaagac 360  
actgggacat acacttgat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420  
gtcaagctca tegtgttgt gcctccatcc aagcctacag ttaacatccc ctctctgcc 480  
accattggga accgggcagt gctgacatgc tcagaacaag atgggtcccc accttctgaa 540  
tacacctggt tcaaagatgg gatagtgat cctacgaatc ccaaaagcac ccgtgccttc 600  
agcaactctt cctatgtcct gaatcccaca acaggagagc tgggtcttga tccccgtca 660  
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720  
tcaaatgctg tgcgcagtga agctgtggag cggaatgtgg gggatcatcg ggcagccgtc 780  
cttghtaacc tgattctcct gggaatcttg gtttttggca tctgggttgc ctatagccga 840  
ggccactttg acagaacaaa gaaagggact tcgagtaaga aggtgattta cagccagcct 900  
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tctagagcgg gaattagagg ctagagcggc tgaaatgggt gtttgggtgat gacactgggg 1440  
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ggagaaaccc tactggaaat acaaagttag ccaggcatgg tgggtgcatgc ctgtagtccc 1800  
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<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile  
1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His  
20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu  
35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe  
50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr  
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe  
85 90 95

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Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser  
                   100                  105                  110  
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val  
                   115                  120                  125  
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr  
                   130                  135                  140  
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro  
 145                  150                  155                  160  
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn  
                   165                  170                  175  
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro  
                   180                  185                  190  
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly  
                   195                  200                  205  
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser  
                   210                  215                  220  
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val  
 225                  230                  235                  240  
 Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly  
                   245                  250                  255  
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly  
                   260                  265                  270  
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu  
                   275                  280                  285  
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val  
                   290                  295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

0905348 07301



<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

50

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

20

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

24

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

20

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

&lt;400&gt; 125

actcagcagt ggtaggaaag

20

&lt;210&gt; 126

&lt;211&gt; 1210

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 126

cagcgcgtgg cccggcgccgc tgtgggggaca gcatgagcgg cggttggatg gcgcaggttg 60  
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctccggactag 120  
gcctggaggc cgcgcgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180  
gctcaggctc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240  
tcacctggcg ctgcgcacagg gacttggact gcagcgatgg cagcgatgag gaggagtgc 300  
ggattgagcc atgtacccag aaagggcaat gccacccgcc ccctggcctc ccctgcccc 360  
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420  
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt cactcacgt 480  
ggcgtgcga cggccaccca gactgtccc actccagcga cgagctcggc tgtggaacca 540  
atgagatcct cccggaagg gatgccacaa ccatggggcc ccctgtgacc ctggagagt 600  
tcacctctct caggaatgcc acaaccatgg ggccccctgt gacctggag agtgtcccc 660  
ctgtcgggaa tgccacatcc tcctctgcc gagaccagtc tggaagccca actgcctatg 720  
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tgtcctggct ccgagcccag gacgcctcc gccactggg gttactggg gccatgaagg 840  
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ccgtcactca gccctgggc tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960  
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ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200  
aagttgcttc 1210

&lt;210&gt; 127

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 127

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80

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T00120-0450660

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<210> 128
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 128
aagttccagt gccgcaccag tggc

<210> 129
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<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129  
 ttggttccac agccgagctc gtcg 24

<210> 130  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130  
 gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc 50

<210> 131  
 <211> 1843  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1837)  
 <223> a, t, c or g

<400> 131  
 cccacgcgtc cgggtctcgct cgctcgcgca gcggcgccag cagaggctgc gcacagatgc 60  
 ggggttagact ggcgggggga ggaggcggag gaggggaagga agctgcatgc atgagaccca 120  
 cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccoga 180  
 gcaatggaga tggatttcta gaggcagcag agcagcagca gcaacctcag tccccccaga 240  
 gactcttggc cgtgatectg tggtttcagc tggcgctgtg ctteggccct gcacagctca 300  
 cgggcggggt cgatgacctt caagtgtgtg ctgaccccg gattcccgag aatggcttca 360  
 ggacccccag cggagggggt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420  
 gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480  
 gctggatccc aagtataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaactg 540  
 aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgct 600  
 atgaaggatt caagatccgg taccgagacc tacacaatat ggtttcatta tgtcgcgatg 660  
 atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720  
 atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780  
 atcgctgctt tcccgattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840  
 ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900  
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09905348.071301

cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200  
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 tggacgacca gagcccccca gcataccccg gctcagggga cacggacaca ggcccagggg 1440  
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 taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680  
 gttgatctgt ggagttgatt ctttcccttc tcttggtttt agacaaatgt aaacaaagct 1740  
 ctgaccccta aaattgctat gctgatagag tggtagaggc tggaagcttg atcaagtcct 1800  
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln  
 1 5 10 15

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val  
 20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr  
 35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu  
 50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val  
 65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys  
 85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser  
 100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu  
 115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile  
 130 135 140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn  
 145 150 155 160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile  
 165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

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			180				185				190				
Ile	Ser	Glu	Leu	Gln	Thr	Ser	Phe	Pro	Val	Gly	Thr	Val	Ile	Ser	Tyr
		195					200					205			
Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys
		210					215					220			
Leu	Gln	Asn	Leu	Ile	Trp	Ser	Ser	Ser	Pro	Pro	Arg	Cys	Leu	Ala	Leu
225					230					235					
Glu	Ala	Gln	Val	Cys	Pro	Leu	Pro	Pro	Met	Val	Ser	His	Gly	Asp	Phe
				245					250					255	
Val	Cys	His	Pro	Arg	Pro	Cys	Glu	Arg	Tyr	Asn	His	Gly	Thr	Val	Val
				260					265					270	
Glu	Phe	Tyr	Cys	Asp	Pro	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Tyr	Lys	Tyr
		275					280					285			
Ile	Thr	Cys	Gln	Tyr	Gly	Glu	Trp	Phe	Pro	Ser	Tyr	Gln	Val	Tyr	Cys
		290					295					300			
Ile	Lys	Ser	Glu	Gln	Thr	Trp	Pro	Ser	Thr	His	Glu	Thr	Leu	Leu	Thr
305					310					315					
Thr	Trp	Lys	Ile	Val	Ala	Phe	Thr	Ala	Thr	Ser	Val	Leu	Leu	Val	Leu
				325					330					335	
Leu	Leu	Val	Ile	Leu	Ala	Arg	Met	Phe	Gln	Thr	Lys	Phe	Lys	Ala	His
				340					345					350	
Phe	Pro	Pro	Arg	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Ser	Asp	Pro	Asp	Phe
				355					360					365	
Val	Val	Val	Asp	Gly	Val	Pro	Val	Met	Leu	Pro	Ser	Tyr	Asp	Glu	Ala
				370					375					380	
Val	Ser	Gly	Gly	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Tyr	Met	Ala	Ser	Val
385					390					395					
Gly	Gln	Gly	Cys	Pro	Leu	Pro	Val	Asp	Asp	Gln	Ser	Pro	Pro	Ala	Tyr
				405					410					415	
Pro	Gly	Ser	Gly	Asp	Thr	Asp	Thr	Gly	Pro	Gly	Glu	Ser	Glu	Thr	Cys
				420					425					430	
Asp	Ser	Val	Ser	Gly	Ser	Ser	Glu	Leu	Leu	Gln	Ser	Leu	Tyr	Ser	Pro
				435					440					445	
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile
				450					455					460	

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

23

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 135

atttaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

cccacgcgtc cgctccgcgc cctccccccc gctctccgtg cggtcgcgtc gtggcctaga 60  
gatgctgctg ccgcggttgc agttgtcgcg cagcctctg cccgccagcc cgctccaccg 120  
ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180  
tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgctgc 240  
tgagtgcctc ggatttgac ctacaggag ggcagccagt ctgccgggga gggacacaga 300

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ggccttggtta taaagtcatt tacttccatg atactttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtcct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatgggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
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gcgaggtctg cgtgggtcatg taccatcagc catcggcacc cgctggcatc ggaggccccct 660
acatgttcca gtggaatgat gaccgggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt ctttctagag aagctgaagg tgaggaaaca gagctgacaa 780
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ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
agcaggaaaa aaaaaa 1815

```

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
100 105 110

0955348 03450550



Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

&lt;210&gt; 138

T02720"84E50660

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attggggtca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaaggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgcgg acttgggggg gcccgcctgag ccccgccgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaaccgcg agggcagcga gggcctacca ccattgatcac 180  
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgct ctgacctcgc tggcgctactg 240  
 cctgcaccag cggcgggttg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg ttctgacacg gggctcggag 360  
 tctctcctcaag ccgctccgcg tggaggagca ggtagagtgg aacccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540  
 gctgaccaag gtgggcatgc agcaaagtgt tgccttggga gagagactga ggaagaacta 600  
 tgtggaagac attcccttcc ttccaccaac cttcaaccca caggaggtct ttattcggtc 660  
 cactaacatt ttctcggaatc tggagtcacac ccgttggttg ctggctgggc ttttccagtg 720

tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgatatcc 780  
 caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840  
 ttacagcca ggaatctcag aggatttgaa aaagggtgaag gacaggatgg gcattgacag 900  
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 cctcccaagc tgcccatgc tgaagagatt tgcacggatg atcgaaacaga gagctgtgga 1020  
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 attcctccac atcctagaga gcaacctgct gaaagccatg gactctgcca ctgccccga 1140  
 caagatcaga aagctgtatc tctatgcggc tcatgatgtg accttcatac cgctcttaat 1200  
 gaccctgggg atttttgacc acaaattggcc acggtttgct gttgacctga ccatggaact 1260  
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 ggtgccgaga ggttgccctg atgggctctg cccgctggac atgttcttga atgccatgtc 1380  
 agtttatacc ttaagcccag aaaaatacca tgcactctgc tctcaaacctc aggtgatgga 1440  
 agttggaat gaagagtaac tgatttataa aagcaggatg tgttgatttt aaaataaagt 1500  
 gcctttatac aatg 1514

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val  
 1 5 10 15

Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala  
 20 25 30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu  
 35 40 45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro  
 50 55 60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu  
 65 70 75 80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu  
 85 90 95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu  
 100 105 110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly  
 115 120 125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val  
 130 135 140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe  
 145 150 155 160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu  
 165 170 175

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Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
 180 185 190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
 195 200 205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
 210 215 220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
 225 230 235 240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
 245 250 255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
 260 265 270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
 275 280 285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
 290 295 300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
 305 310 315 320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
 325 330 335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
 340 345 350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
 355 360 365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
 370 375 380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
 385 390 395 400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
 405 410 415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
 420 425

&lt;210&gt; 143

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

0905348-071301  
 106720-84250660

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145

tccttcccgt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
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ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

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gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
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ggtcctcatc caatcagtc gttgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattgtt cacatgatga agatgctggg gcatcgtgtg agaaccaga 480
gagctctttc tccccagtc cagagggtgt caggctggct gacggccctg ggcattgcaa 540
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cctccggggc gcaaagggtg tgtgccggca gctgggatgt gggagggtg tactgactca 660
aaaacgctgc aacaagcatg cctatggcgc aaaacccatc tggctgagcc agatgtcatg 720
ctcaggacga gaagcaaccc ttcaggattg cccttctggg ccttggggga agaacacctg 780
caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840
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tgthtctctg aagaactctg acaaaatata gattttggta ctgaaagaga ttctagagga 1560
acggaatttt aaggataaat tttctgaatt gggttatggg tttctgaaat tggctctata 1620
atctaattag atataaaatt ctggtaactt tatttacaat aataaagata gcactatgtg 1680
ttcaaa 1686

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<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
100 105 110

TEXT-20" BHE50550

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu  
 115 120 125  
 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro  
 130 135 140  
 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr  
 145 150 155 160  
 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys  
 165 170 175  
 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn  
 180 185 190  
 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys  
 195 200 205  
 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly  
 210 215 220  
 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp  
 225 230 235 240  
 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg  
 245 250 255  
 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn  
 260 265 270  
 Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly  
 275 280 285  
 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly  
 290 295 300  
 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln  
 305 310 315 320  
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr  
 325 330 335  
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val  
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

0905348-07.1301

## oligonucleotide probe

&lt;400&gt; 149

ttcagctcat caccttcacc tgcc

24

&lt;210&gt; 150

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 150

ggctcataca aaataccact aggg

24

&lt;210&gt; 151

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

&lt;210&gt; 152

&lt;211&gt; 1427

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 152

actgcactcg gttctatcga ttgaattccc cggggatcct ctagagatcc ctgcacctcg 60  
 acccacgcgt ccgcggacgc gtggcgaggc gcgtgggccc gctaccagga agagtctgcc 120  
 gaaggatgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180  
 cctgggcgtc ttccgacctc tccggtctgt gcagtgggtg cgcgggaagg cctacctgcg 240  
 gaatgctgtg gtggtgatca caggcgccac ctgaggctg ggcaaagaat gtgcaaaagt 300  
 cttctatgct gcgggtgcta aactggtgct ctgtggcccg aatggtgggg ccctagaaga 360  
 gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420  
 ggtgaccttc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480  
 gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540  
 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccgagt 600  
 tgctctaacy aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660  
 catcagcagc atccagggca agatgagcat tccttttcca tcagcatatg cagcctccaa 720  
 gcacgcaacc caggctttct ttgactgtct gcgtgcccag atggaacagt atgaaattga 780  
 ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaagt ccatcaccgc 840  
 ggatggatct aggtatggag ttatggacac caccacagcc caggggccgaa gccctgtgga 900  
 ggtggcccgag gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960  
 cttactgcct tccttggtcg tttatcttcg aactctggct cctgggctct tcttcagcct 1020  
 catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080

090548-07301



agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140  
 ttgttgagac tttaatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200  
 gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc caggggtgagg 1260  
 ggaaacactt aaggaataaa tatggagctg ggggtttaaca ctaaaaacta gaaataaaca 1320  
 tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380  
 cttggccgcc atggcccaac ttgtttattg cagcttataa tggttac 1427

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys  
 1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys  
 20 25 30

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly  
 35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu  
 50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu  
 65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu  
 85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala  
 100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala  
 115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp  
 130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys  
 145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala  
 165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr  
 180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala  
 195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210                                      215                                      220  
 Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg  
 225                                      230                                      235                                      240  
 Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu  
                                     245                                      250                                      255  
 Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val  
                                     260                                      265                                      270  
 Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu  
                                     275                                      280                                      285  
 Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu  
                                     290                                      295                                      300  
 Arg Lys Ser Lys Asn Ser  
 305                                      310

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 154

ggtgctaaac tgggtgctctg tggc

24

<210> 155

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 155

cagggcaaga tgagcattcc

20

<210> 156

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

TOEFTD"84E50660

<400> 156  
tcatactgtt ccatctcggc acgc

24

<210> 157  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157  
aatggtgggg ccctagaaga gctcatcaga gaactcacgc cttctcatgc

50

<210> 158  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 158  
cccacgcgtc cgctgggtgtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60  
aaaaaaaaaa acacacccaaa cgctcgcagc cacaaaaggg atgaaatttc ttctggacat 120  
cctcctgctt ctcccgttac tgatcgtctg ctccctagag tccttcgtga agctttttat 180  
tcctaagagg agaaaatcag tcaccggcga aatcgtgctg attacaggag ctgggcatgg 240  
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300  
tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg gtgccaaggt 360  
tcataccttt gtggttagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420  
gaaggcagaa attggagatg ttagtatttt agtaataat gctgggtgtg tctatacatc 480  
agatttggtt gctacacaag atcctcagat tgaaaagact tttgaagtta atgtacttgc 540  
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tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660  
aagcaagttt gctgctgttg gatttcataa aactttgaca gatgaactgg ctgccttaca 720  
aataactgga gtcaaaaaca catgtctgtg tctaatttc gtaaacactg gcttcatcaa 780  
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tcatttacta ccacttggtc tttagccaaa agctgattac atatgatata aacagagaaa 1200  
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agagaatgta cccacaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaa 1680  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a a 1771

<210> 159

090549-01301

<213> Homo sapiens

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val  
1 5 10 15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys  
20 25 30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile  
35 40 45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val  
50 55 60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys  
65 70 75 80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn  
85 90 95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly  
100 105 110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp  
115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn  
130 135 140

Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
145					150					155					160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His  
165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala  
180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile  
195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly  
210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu  
225 230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met  
245 250 255

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile  
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys  
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln  
 290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 161

atcccatgca tcagcctggt tacc

24

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 162

gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

cccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60  
 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaagggtg 120

0905348.0450660

attgttttcgc tggctcctggt gatgcctggc ccctgtgatg ggctgttttcg ctccctatac 180  
 agaagtgttt ccatgccacc taagggagac tcaggacagc cattatttct cacccttac 240  
 attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggtcggccc tttcccagga 300  
 ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360  
 ttctttctggt tcttcccagc tcagatacag ccagaagatg cccagtagt tctctggcta 420  
 caggggtgggc cgggaggttc atccatgttt ggactctttg tggaaacatgg gccttatgtt 480  
 gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540  
 ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600  
 gcagtcaatg aggacgatgt agcacgggat ttatacagtg cactaattca gtttttccag 660  
 atatttcctg aatataaaaa taatgacttt tatgtcactg gggagtctta tgcagggaaa 720  
 tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780  
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 aagcagtgcc atgaatgcat agaacacatc aggaagcaga actgggtttga ggcttttgaa 960  
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 acaggatgta gtaattacta taactttttg cgggtgcacgg aacctgagga tcagctttac 1080  
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 aaaggatggg atccttatgt tggataaact accttcccaa aagagaacat cagagggtttt 1560  
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 tcatatctgc aagatttttt tcatcaataa aaattatcct tgaaacaagt gagcttttgt 1680  
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 ttaacttaaa ggatgaaagg tatggatgat gtgacactga gacaagatgt ataaatgaaa 1800  
 ttttaggggtc ttgaatagga agtttttaatt tcttctaaga gtaagtgaaa agtgcagttg 1860  
 taacaaacaa agctgtaaca tctttttctg ccaataacag aagtttggca tgccgtgaag 1920  
 gtgttttgaa atattattgg ataagaatag ctcaattatc ccaataaaat ggatgaagct 1980  
 ataatagttt tggggaaaaag attctcaaat gtataaagtc ttagaacaaa agaattcttt 2040  
 gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met  
 1 5 10 15

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser  
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr  
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly  
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

090543-07131

65		70		75		80
Asn Lys Thr Tyr	Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln					
	85		90			95
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro						
	100		105			110
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val						
	115		120			125
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr						
	130		135			140
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser						
	145		150			155
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala						
			165			170
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu						
			180			185
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys						
			195			200
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg						
			210			215
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser						
			225			230
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile						
			245			250
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His						
			260			265
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu						
			275			280
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr						
			290			295
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys						
			305			310
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro						
			325			330
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly						
			340			345
						350

0905348-071301

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 165

ttccatgcca cctaagggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

0905348.04E50660



&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 167

agctctcaga ggctggcat aggg

24

&lt;210&gt; 168

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 168

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttctcac

50

&lt;210&gt; 169

&lt;211&gt; 2477

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

cgagggtctt tccggctccg gaatggcaca tgtgggaatc ccagtcttgt tggctacaac 60  
 atttttccct ttcttaacaa gttctaacag ctgttctaac agctagtgat caggggttct 120  
 tcttgctgga gaagaaaggg ctgagggcag agcagggcac tctcactcag ggtgaccagc 180  
 tcttgctcctc tctgtggata acagagcatg agaaagtga gagatgcagc ggagtggagt 240  
 gatggaagtc taaaatagga aggaattttg tgtgcaatat cagactctgg gagcagttga 300  
 cctggagagc ctgggggagg gcctgcctaa caagctttca aaaaacagga ggcacttcca 360  
 ctgggctggg ataagacgtg ccggtaggat agggaagact gggtttagtc ctaatatcaa 420  
 attgactggc tgggtgaact tcaacagcct tttaacctct ctgggagatg aaaacgatgg 480  
 cttaaggggc cagaaataga gatgctttgt aaaataaaat tttaaaaaaa gcaagtattt 540  
 tatagcataa aggctagaga ccaaaataga taacaggatt ccctgaacat tcctaagagg 600  
 gagaaagtat gttaaaaata gaaaaaccaa aatgcagaag gaggagactc acagagctaa 660  
 accaggatgg ggaccctggg tcaggccagc ctctttgctc ctcccggaaa ttatttttgg 720  
 tctgaccact ctgccttggt ttttgagaa tcatgtgagg gccaaaccggg gaagggtggag 780  
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 aatcgtgact ggaccttcaa ccacttgacc gtccaccaag ggacgggggc cgtctatgtg 1020  
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 ctcatcaaga tcccttcaga caccctggcc ctgggtctccc actttgacat cttctacatc 1560  
 tacggctttg ctagtggggg ctttgtctac tttctcactg tccagcccga gaccctgag 1620  
 ggtgtggcca tcaactccgc tggagacctc ttctacacct cagcctcgt gcggctctgc 1680

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F01E20-BHE50660

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gccttcaata tcaccagcca ggacgatgta ctctttgcca tcttctccaa agggcagaag 1860  
cagtatcacc acccgcccga tgactctgcc ctgtgtgcct tccctatccg ggccatcaac 1920  
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aggggttaat tttgtgactt agcttctagc tacttccctc agccatcagt cattgggtat 2400  
gtaaggaatg caagcgattt tcaatatttc ccaaacttta agaaaaaact ttaagaaggt 2460  
acatctgcaa aagcaaa 2477

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr  
1 5 10 15

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly  
20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu  
35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala  
50 55 60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val  
65 70 75 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His  
85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly  
100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr  
115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp  
130 135 140

Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val  
145 150 155 160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser  
165 170 175

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Glu	Asn	Arg	Leu	Leu	Ala	Cys	Gly	Ser	Leu	Tyr	Gln	Gly	Val	Cys	Lys
			180				185						190		
Leu	Leu	Arg	Leu	Asp	Asp	Leu	Phe	Ile	Leu	Val	Glu	Pro	Ser	His	Lys
			195				200						205		
Lys	Glu	His	Tyr	Leu	Ser	Ser	Val	Asn	Lys	Thr	Gly	Thr	Met	Tyr	Gly
			210				215						220		
Val	Ile	Val	Arg	Ser	Glu	Gly	Glu	Asp	Gly	Lys	Leu	Phe	Ile	Gly	Thr
			225				230						235		
Ala	Val	Asp	Gly	Lys	Gln	Asp	Tyr	Phe	Pro	Thr	Leu	Ser	Ser	Arg	Lys
			245							250			255		
Leu	Pro	Arg	Asp	Pro	Glu	Ser	Ser	Ala	Met	Leu	Asp	Tyr	Glu	Leu	His
			260				265						270		
Ser	Asp	Phe	Val	Ser	Ser	Leu	Ile	Lys	Ile	Pro	Ser	Asp	Thr	Leu	Ala
			275				280						285		
Leu	Val	Ser	His	Phe	Asp	Ile	Phe	Tyr	Ile	Tyr	Gly	Phe	Ala	Ser	Gly
			290				295						300		
Gly	Phe	Val	Tyr	Phe	Leu	Thr	Val	Gln	Pro	Glu	Thr	Pro	Glu	Gly	Val
			305							315			320		
Ala	Ile	Asn	Ser	Ala	Gly	Asp	Leu	Phe	Tyr	Thr	Ser	Arg	Ile	Val	Arg
			325							330			335		
Leu	Cys	Lys	Asp	Asp	Pro	Lys	Phe	His	Ser	Tyr	Val	Ser	Leu	Pro	Phe
			340				345						350		
Gly	Cys	Thr	Arg	Ala	Gly	Val	Glu	Tyr	Arg	Leu	Leu	Gln	Ala	Ala	Tyr
			355				360						365		
Leu	Ala	Lys	Pro	Gly	Asp	Ser	Leu	Ala	Gln	Ala	Phe	Asn	Ile	Thr	Ser
			370				375						380		
Gln	Asp	Asp	Val	Leu	Phe	Ala	Ile	Phe	Ser	Lys	Gly	Gln	Lys	Gln	Tyr
			385				390						395		
His	His	Pro	Pro	Asp	Asp	Ser	Ala	Leu	Cys	Ala	Phe	Pro	Ile	Arg	Ala
			405							410			415		
Ile	Asn	Leu	Gln	Ile	Lys	Glu	Arg	Leu	Gln	Ser	Cys	Tyr	Gln	Gly	Glu
			420				425						430		
Gly	Asn	Leu	Glu	Leu	Asn	Trp	Leu	Leu	Gly	Lys	Asp	Val	Gln	Cys	Thr
			435				440						445		
Lys	Ala	Pro	Val	Pro	Ile	Asp	Asp	Asn	Phe	Cys	Gly	Leu	Asp	Ile	Asn

450                      455                      460  
 Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr  
 465                      470                      475                      480  
 Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly  
                     485                      490                      495  
 Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val  
                     500                      505                      510  
 Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys  
                     515                      520                      525  
 Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln  
                     530                      535                      540  
 Leu Tyr Phe Leu Gly Glu Gln Arg  
 545                      550

<210> 171

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 171

tggaataaccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 172

cttctgccct ttggagaaga tggc

24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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F0E72D-B4E50660

<400> 173  
ggactcactg gccaggcct tcaatatcac cagccaggac gat

42

<210> 174  
<211> 3106  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1683)  
<223> a, t, c or g

<400> 174  
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aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120  
tgctggctcg cttgggcttc ctgggtgctcc gcaggctgga ctggagcacc ctgggccctc 180  
tgcggtcccg ccatcgacag ctggggctgc aggccaaggg ctggaacttc atgctggagg 240  
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aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgctg ccaggccccct 480  
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ggatggctct gggcctggct ttgttgatga tggctttcct acagccctgc tcttgtgccg 2220  
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TOTAL 208450660

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 gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac acctggcttg 3060  
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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD\_RES

<222> (539)

<223> Any amino acid

<400> 175

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu  
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Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp  
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Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln  
 35 40 45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe  
 50 55 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp  
 65 70 75 80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr  
 85 90 95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser  
 100 105 110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly  
 115 120 125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp  
 130 135 140

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Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
 145 150 155 160  
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175  
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
 180 185 190  
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
 195 200 205  
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
 210 215 220  
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly  
 225 230 235 240  
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu  
 245 250 255  
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro  
 260 265 270  
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
 275 280 285  
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
 290 295 300  
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
 305 310 315 320  
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
 325 330 335  
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
 340 345 350  
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
 355 360 365  
 Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro  
 370 375 380  
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
 385 390 395 400  
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
 405 410 415  
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
 420 425 430

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Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

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aaggggagca aagccgggct cggcccagg cccccaggac ctccatctcc caatgttga 180  
ggaatccgac acgtgacggt ctgtccgccg tctcagacta gaggagcgct gtaaaccgcca 240  
tggtcccaa gaagctgtcc tgcttcggtt ccctgctgct gccgctcagc ctgacgctac 300  
tgctgcccc ggcagacact cggtcgttcg tagtggatag gggtcacgac cggtttctcc 360  
tagacggggc cccgttcgcg tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

090543E3720"34E50660



tgctttgggc cgaccggctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480  
 atgtgccctg gaactaccac gagccacagc ctgggggtcta taactttaat ggcagccggg 540  
 acctcattgc ctttctgaat gaggcagctc tagcgaacct gttgggtcata ctgagaccag 600  
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 ctgtgtcagc tgtaaccaa ggactagaga acatgctcaa gttgggagcc agtgtgaaca 1140  
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 cccataccat ttttgagcca acaccattct ggggtccaaa taatggagtc catgaccgtg 1560  
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 actccaaaac atttccaatt ttaggctcag ttggggacac atttctatat ctacctggat 1920  
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<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu  
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Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val  
 20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr  
 35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala  
 50 55 60

Asp	Arg	Leu	Leu	Lys	Met	Arg	Trp	Ser	Gly	Leu	Asn	Ala	Ile	Gln	Phe	65	70	75	80
Tyr	Val	Pro	Trp	Asn	Tyr	His	Glu	Pro	Gln	Pro	Gly	Val	Tyr	Asn	Phe	85	90	95	
Asn	Gly	Ser	Arg	Asp	Leu	Ile	Ala	Phe	Leu	Asn	Glu	Ala	Ala	Leu	Ala	100	105	110	
Asn	Leu	Leu	Val	Ile	Leu	Arg	Pro	Gly	Pro	Tyr	Ile	Cys	Ala	Glu	Trp	115	120	125	
Glu	Met	Gly	Gly	Leu	Pro	Ser	Trp	Leu	Leu	Arg	Lys	Pro	Glu	Ile	His	130	135	140	
Leu	Arg	Thr	Ser	Asp	Pro	Asp	Phe	Leu	Ala	Ala	Val	Asp	Ser	Trp	Phe	145	150	155	160
Lys	Val	Leu	Leu	Pro	Lys	Ile	Tyr	Pro	Trp	Leu	Tyr	His	Asn	Gly	Gly	165	170	175	
Asn	Ile	Ile	Ser	Ile	Gln	Val	Glu	Asn	Glu	Tyr	Gly	Ser	Tyr	Arg	Ala	180	185	190	
Cys	Asp	Phe	Ser	Tyr	Met	Arg	His	Leu	Ala	Gly	Leu	Phe	Arg	Ala	Leu	195	200	205	
Leu	Gly	Glu	Lys	Ile	Leu	Leu	Phe	Thr	Thr	Asp	Gly	Pro	Glu	Gly	Leu	210	215	220	
Lys	Cys	Gly	Ser	Leu	Arg	Gly	Leu	Tyr	Thr	Thr	Val	Asp	Phe	Gly	Pro	225	230	235	240
Ala	Asp	Asn	Met	Thr	Lys	Ile	Phe	Thr	Leu	Leu	Arg	Lys	Tyr	Glu	Pro	245	250	255	
His	Gly	Pro	Leu	Val	Asn	Ser	Glu	Tyr	Tyr	Thr	Gly	Trp	Leu	Asp	Tyr	260	265	270	
Trp	Gly	Gln	Asn	His	Ser	Thr	Arg	Ser	Val	Ser	Ala	Val	Thr	Lys	Gly	275	280	285	
Leu	Glu	Asn	Met	Leu	Lys	Leu	Gly	Ala	Ser	Val	Asn	Met	Tyr	Met	Phe	290	295	300	
His	Gly	Gly	Thr	Asn	Phe	Gly	Tyr	Trp	Asn	Gly	Ala	Asp	Lys	Lys	Gly	305	310	315	320
Arg	Phe	Leu	Pro	Ile	Thr	Thr	Ser	Tyr	Asp	Tyr	Asp	Ala	Pro	Ile	Ser	325	330	335	
Glu	Ala	Gly	Asp	Pro	Thr	Pro	Lys	Leu	Phe	Ala	Leu	Arg	Asp	Val	Ile				

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	340		345		350										
Ser	Lys	Phe	Gln	Glu	Val	Pro	Leu	Gly	Pro	Leu	Pro	Pro	Pro	Ser	Pro
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Lys	Met	Met	Leu	Gly	Pro	Val	Thr	Leu	His	Leu	Val	Gly	His	Leu	Leu
	370					375					380				
Ala	Phe	Leu	Asp	Leu	Leu	Cys	Pro	Arg	Gly	Pro	Ile	His	Ser	Ile	Leu
385					390					395					400
Pro	Met	Thr	Phe	Glu	Ala	Val	Lys	Gln	Asp	His	Gly	Phe	Met	Leu	Tyr
				405					410					415	
Arg	Thr	Tyr	Met	Thr	His	Thr	Ile	Phe	Glu	Pro	Thr	Pro	Phe	Trp	Val
			420					425					430		
Pro	Asn	Asn	Gly	Val	His	Asp	Arg	Ala	Tyr	Val	Met	Val	Asp	Gly	Val
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Phe	Gln	Gly	Val	Val	Glu	Arg	Asn	Met	Arg	Asp	Lys	Leu	Phe	Leu	Thr
	450					455					460				
Gly	Lys	Leu	Gly	Ser	Lys	Leu	Asp	Ile	Leu	Val	Glu	Asn	Met	Gly	Arg
465					470					475					480
Leu	Ser	Phe	Gly	Ser	Asn	Ser	Ser	Asp	Phe	Lys	Gly	Leu	Leu	Lys	Pro
				485					490					495	
Pro	Ile	Leu	Gly	Gln	Thr	Ile	Leu	Thr	Gln	Trp	Met	Met	Phe	Pro	Leu
			500					505					510		
Lys	Ile	Asp	Asn	Leu	Val	Lys	Trp	Trp	Phe	Pro	Leu	Gln	Leu	Pro	Lys
		515					520					525			
Trp	Pro	Tyr	Pro	Gln	Ala	Pro	Ser	Gly	Pro	Thr	Phe	Tyr	Ser	Lys	Thr
	530					535					540				
Phe	Pro	Ile	Leu	Gly	Ser	Val	Gly	Asp	Thr	Phe	Leu	Tyr	Leu	Pro	Gly
545					550					555					560
Trp	Thr	Lys	Gly	Gln	Val	Trp	Ile	Asn	Gly	Phe	Asn	Leu	Gly	Arg	Tyr
				565					570					575	
Trp	Thr	Lys	Gln	Gly	Pro	Gln	Gln	Thr	Leu	Tyr	Val	Pro	Arg	Phe	Leu
			580					585					590		
Leu	Phe	Pro	Arg	Gly	Ala	Leu	Asn	Lys	Ile	Thr	Leu	Leu	Glu	Leu	Glu
		595					600					605			
Asp	Val	Pro	Leu	Gln	Pro	Gln	Val	Gln	Phe	Leu	Asp	Lys	Pro	Ile	Leu
	610					615					620				

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22

<210> 182  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 182  
 tggcaccag aatggtgtg gctc

24

<210> 183  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 183  
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc

50

<210> 184  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

<400> 184  
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 gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cctttgaagg 180  
 aatattcttt cgaaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240  
 acgatttttg gttccttctt cacatggtag accagtatga ccagctatat tccaagcggt 300  
 ttggtgtgtt cttgtcagaa gttagtgaata ataaacttag ggaaattagt ttgaaccatg 360  
 agtggacatt tgaaaaactc aggcagcaca ttacacgcaa cgcccaggac aagcaggagt 420  
 tgcactctgt catgctgtcg ggggtgccc atgctgtctt tgacctcaca gacctggatg 480  
 tgctaaagct tgaactaatt ccagaagcta aaattcctgc taagatttct caaatgacta 540  
 acctccaaga gctccacctc tgccactgcc ctgcaaaaagt tgaacagact gcttttagct 600  
 ttcttcgcga tcacttgaga tgccctcacg tgaagttcac tgatgtggct gaaattcctg 660  
 cctgggtgta tttgctcaaa aaccttcgag agttgtactt aataggcaat ttgaactctg 720  
 aaaacaataa gatgatagga cttgaatctc tccgagagtt gcggcacctt aagattctcc 780  
 acgtgaagag caatttgacc aaagttccct ccaacattac agatgtggct ccacatctta 840  
 caaagttagt cattcataat gacggcacta aactcttggt actgaacagc ctttaagaaa 900  
 tgatgaatgt cgctgagctg gaactccaga actgtgagct agagagaatc ccacatgcta 960  
 ttttcagcct ctctaattta caggaaactgg atttaaagtc caataacatt cgcacaattg 1020  
 aggaaatcat cagtttccag catttaaaac gactgacttg tttaaaatta tggcataaca 1080  
 aaattgttac tattcctccc tctattaccc atgtcaaaaa cttggagtca ctttatttct 1140  
 ctaacaacaa gctcgaatcc ttaccagtgg cagtatttag ttacagaaa ctcagatgct 1200  
 tagatgtgag ctacaacaac atttcaatga ttccaataga aataggattg cttcagaacc 1260  
 tgcagcattt gcatatcact gggaacaaag tggacattct gccaaaacaa ttgttttaaa 1320

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gcataaagtt gaggactttg aatctgggac agaactgcat cacctcactc ccagagaaag 1380
ttggtcagct ctcccagctc actcagctgg agctgaaggg gaactgcttg gaccgcctgc 1440
cagcccagct gggccagtgt cggatgctca agaaaagcgg gcttggttg gaagatcacc 1500
tttttgatac cctgccactc gaagtcaaag aggcattgaa tcaagacata aatattccct 1560
ttgcaaagtg gatttaaact aagataatat atgcacagtg atgtgcagga acaacttcct 1620
agattgcaag tgctcacgta caagttatta caagataatg catttttagga gtagatacat 1680
cttttaaaat aaaacagaga ggatgcatag aaggctgata gaagacataa ctgaatgttc 1740
aatgtttgta gggttttaag tcattcattt ccaaatacatt ttttttttc ttttggggaa 1800
aggggaaggaa aaattataat cactaatctt gggtcttttt aaattgtttg taacttggat 1860
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ttttcttact aaaaaaaaaa aaaaaaa 1947

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<210> 185  
 <211> 501  
 <212> PRT  
 <213> Homo sapiens

<400> 185

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			20					25					30		
Ile	Pro	Leu	Lys	Glu	Tyr	Ser	Phe	Glu	Lys	Val	Arg	Glu	Glu	Ser	Ser
		35					40					45			
Phe	Ser	Asp	Ile	Pro	Asp	Val	Lys	Asn	Asp	Phe	Ala	Phe	Leu	Leu	His
	50					55					60				
Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe
65					70					75				80	
Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His
				85					90					95	
Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	His	Ile	Ser	Arg	Asn	Ala	Gln
		100					105						110		
Asp	Lys	Gln	Glu	Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala
		115					120					125			
Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro
	130					135					140				
Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu
145					150					155				160	
Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser
			165						170					175	
Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val
		180					185						190		

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Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205  
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220  
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240  
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255  
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270  
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285  
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300  
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320  
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335  
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350  
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365  
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380  
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400  
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415  
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430  
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445  
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460  
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

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TDE F20" BHE50550

465                                      470                                      475                                      480

Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro

                                    485                                      490                                      495

Phe Ala Asn Gly Ile

                                    500

<210> 186  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 186  
 cctccctcta ttacccatgt c 21

<210> 187  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 187  
 gaccaacttt ctctgggagt gagg 24

<210> 188  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 188  
 gtcactttat ttctctaaca acaagctcga atccttacca gtggcag 47

<210> 189  
 <211> 2917  
 <212> DNA  
 <213> Homo sapiens

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TOE T 20 " 24E50660



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&lt;211&gt; 607

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

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Cys	Leu	Ala	Glu	Leu	Thr	Met	Ala	Glu	Ala	Glu	Gly	Asn	Ala	Ser	Cys	20	25	30	
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Ile	Leu	Gln	Leu	Asn	Pro	Ser	Glu	Asn	Cys	Thr	Trp	Thr	Ile	Glu	Arg	50	55	60	
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Pro	Asp	Gly	Ser	Cys	Glu	Ser	Glu	Asn	Ile	Lys	Val	Phe	Asp	Gly	Thr	85	90	95	
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Thr	Asp	Ser	Ala	Arg	Ile	Gln	Arg	Thr	Val	Phe	Val	Phe	Tyr	Tyr	Phe	130	135	140	
Phe	Ser	Pro	Asn	Ile	Ser	Ile	Pro	Asn	Cys	Gly	Gly	Tyr	Leu	Asp	Thr	145	150	155	160
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Lys	Leu	Asn	Phe	Lys	Glu	Ile	Phe	Leu	Glu	Ile	Asp	Lys	Gln	Cys	Lys	195	200	205	
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<213> Homo sapiens

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Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala  
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 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
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Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
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Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
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Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
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Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
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<210> 198

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<213> Artificial sequence

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Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
          85                      90                      95

```

```

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
          100                      105                      110

```

```

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
          115                      120                      125

```

```

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
          130                      135                      140

```

T00120-34E50660

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

09905348-071304

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 203

gtcagtgaca gtacctactc gg

22

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 204

tggagcagga ggagtagtag tagg

24

<210> 205

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 205

aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<210> 206

<211> 1620

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (973)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (977)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (996)

<223> a, t, c or g

<220>

<221> modified\_base

0905348-0130

&lt;222&gt; (1003)

&lt;223&gt; a, t, c or g

&lt;400&gt; 206

```

agatggcggt cttggcacct ctaattgctc tcgtgtatcc ggtgcgcgga ctttcacgat 60
ggctcgccca accttactac cttctgtcgg ccctgctctc tgctgccttc ctactcgtga 120
ggaaactgcc gccgctctgc caccgtctgc ccacccaacg cgaagacggt aaccctgtg 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccattgtg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
ccaacacaat tcttttcttc cgcttgataa ttgcgatggg cctactttac atcacactct 360
gcatagtgtt cctgatgacg tgcaaacccc ccctatatat gggccctgag tatatcaagt 420
acttcaatga taaaaccatt gatgaggaac tagaacggga caagaggggtc acttggattg 480
tggagttctt tgccaattgg tctaattgact gccaatcatt tgcccctatc tatgctgacc 540
tctcccttaa atacaactgt acagggctaa attttgggaa ggtggatgtt ggacgctata 600
ctgatgttag tacgcggtac aaagtgagca catcaccctc caccaagcaa ctccctaccc 660
tgatcctgtt ccaaggtggc aaggaggcaa tgccggcgcc acagattgac aagaaaggac 720
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tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gacgagcctg 840
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actttccttt gtgtggtagg acttggagga gaaatccctt ggactttcac taacctctg 1560
acatactccc cacaccagat tgatggcttt ccgtaataaa aagattggga tttcctttt 1620

```

&lt;210&gt; 207

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

```

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
  1             5             10             15

```

```

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
      20             25             30

```

```

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
      35             40             45

```

```

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
      50             55             60

```

```

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
      65             70             75             80

```

T.D.E.T. 40-84E0660

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
                             85                            90                            95  
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
                             100                            105                            110  
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
                             115                            120                            125  
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
                             130                            135                            140  
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
                             145                            150                            155                            160  
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
                             165                            170                            175  
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
                             180                            185                            190  
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
                             195                            200                            205  
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
                             210                            215                            220  
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
                             225                            230                            235                            240  
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
                             245                            250                            255  
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
                             260                            265                            270  
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
                             275                            280                            285  
 Asp Gly Glu Asn Lys Lys Asp Lys  
                             290                            295

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 208

gcttgatat tcgcatgggc ctac

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg

20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 210  
 aacagttggc cacagcatgg cagg

24

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 211  
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag

50

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212

ggacagctcg cggcccccca gagctctagc cgtcgaggag ctgcctgggg acgtttgccc 60  
 tggggcccca gcctggcccg ggtcaccctg gcatgaggag atgggcctgt tgctcctggt 120  
 cccattgctc ctgctgcccg gtcctacgg actgcccttc tacaacggct tctactactc 180  
 caacagcgcc aacgaccaga acctaggcaa cggatcatggc aaagacctcc ttaatggagt 240  
 gaagctgggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300  
 cctgccctgc cgctaccgct acgagccggc cctgggtctcc ccgcggcgtg tgcgtgtcaa 360  
 atgggtggaag ctgtcggaga acggggcccc agagaaggac gtgctggtgg ccatcgggct 420  
 gaggcaccgc tcctttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480  
 tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540  
 ggtcattgac gggctggagg atgaaagcgg tctggtggag ctggagctgc ggggtgtggt 600

0905348.01301

ctttccttac cagtccccca acgggcgcta ccagttcaac ttccacgagg gccagcaggt 660  
 ctgtgcagag caggctgcgg tggtagcctc ctttgagcag ctcttcggg cctgggagga 720  
 gggcctggac tggtagaacg cgggctggct gcaggatgct acgggtgcagt accccatcat 780  
 gttgccccgg cagccctgcg gtggcccagg cctggcacct ggcgtagcga gctacggccc 840  
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 ggtgtactac ctggagcacc ctgagaagct gacgtgcaca gaggcaaggg aggcctgcc 960  
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 agccatttta actgttttta tacttctcaa tttaaatttt ctttaaacad ttttttacta 1320  
 ttttttgtaa agcaaacaga acccaatgcc tccctttgct cctggatgcc ccactccagg 1380  
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 agaatgccgc cgggagtcg ggcattgtgg gcacagttct ccctgcccc cagcctgggg 1560  
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 aggggcccc aggtgtgtgt actttggaca ataatggtg ctatgactgc cttccgccc 1860  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1920  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980  
 aaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met Gly Leu Leu Leu Val Pro Leu Leu Leu Pro Gly Ser Tyr

1 5 10 15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp

20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys

35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala

50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser

65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala

85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe

100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

TOE120" BHE5050

115	120	125
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr		
130	135	140
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu		
145	150	155
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg		
	165	170
		175
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala		
	180	185
		190
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly		
	195	200
		205
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr		
	210	215
		220
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro		
225	230	235
		240
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp		
	245	250
		255
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu		
	260	265
		270
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu		
	275	280
		285
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys		
	290	295
		300
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser		
305	310	315
		320
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu		
	325	330
		335
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr		
	340	345
		350
Gly Val Tyr Cys Tyr Arg Gln His		
	355	360

&lt;210&gt; 214

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

0905348.071304



<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 215

ttcccttgtg ggttgag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 216

agggctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 217

agccagtgag gaaatgag

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 218

tgtccaaagt acacacacct gagg

24

TOCT20"34E50660

<210> 219  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 219  
 gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220  
 <211> 1503  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
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 gcttctgttg ctactgaggc acggggccca ggggaagcca tcccagacg caggccctca 120  
 tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctcccatg atgacgcca 180  
 cgggaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240  
 ccaactcacc ccagaggaaa gccaggcccc tctggggcgg atcgtggacc gcatggaccg 300  
 cgcgggggac ggcgacggct ggggtgtcgt ggcgagctt cgcgcgtgga tcgcgcacac 360  
 gcagcagcgg cacatacggg actcgggtgag cgcggcctgg gacacgtacg acacggaccg 420  
 cgacgggcgt gtgggttggg aggagctgcg caacgccacc tatggccact acgcgcccgg 480  
 tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctcgggacga 540  
 gcggcggttc cgggtggccg accaggatgg ggactcgatg gccactcgag aggagctgac 600  
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 gtactcagcc gagcctgggg aggaggagcc ggcgtgggtg cagacggaga ggcagcagtt 780  
 ccgggacttc cgggatctga acaaggatgg gcacctggat gggagtgagg tgggccactg 840  
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 cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctgggtaatt ggaacatgtt 960  
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 cagctccaaa tctgagcctc caccacatag actgaaactc ccctggcccc agccctctcc 1380  
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 accttgaanaa 1500  
 aaa 1503

<210> 221  
 <211> 328  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
 Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

FOR "A" 24250650

1	5	10	15
Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly	20	25	30
Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala	35	40	45
His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val	50	55	60
Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu	65	70	75
Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp	85	90	95
Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg	100	105	110
His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp	115	120	125
Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly	130	135	140
His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr	145	150	155
Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp	165	170	175
Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu	180	185	190
His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr	195	200	205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu	210	215	220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala	225	230	235
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn	245	250	255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro	260	265	270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu	275	280	285

09505348-071301

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

TOE T 20 24 E 50 65 0

<400> 225  
 cccccctgag cgacgctccc ccatgatgac gcccacggga actt

44

<210> 226  
 <211> 2403  
 <212> DNA  
 <213> Homo sapiens

<400> 226  
 ggggccttgc cttccgcact cgggcgcagc cgggtggatc tcgagcaggt gcggagcccc 60  
 gggcggcggg cgcgggtgcg agggatccct gacgcctctg tccctgtttc tttgtcgctc 120  
 ccagcctgtc tgtcgctcgtt ttggcgcccc cgccctcccc cggtgcgggg ttgcacaccg 180  
 atcctgggct tcgctcgatt tgccgcgcag gcgcctccca gacctagagg ggcgctggcc 240  
 tggagcagcg ggtcgtctgt gtccctctct ctctgcgcgc cgcccgggga tccgaagggt 300  
 gcggggctct gaggaggtga cgcgcggggc ctcccgcacc ctggccttgc ccgcattctc 360  
 cctctctccc aggtgtgagc agcctatcag tcaccatgtc cgcagcctgg atcccggctc 420  
 tcggcctcgg tgtgtgtctg ctgctgctgc cggggccccg gggcagcgag ggagccgctc 480  
 ccattgctat cacatgtttt accagaggct tggacatcag gaaagagaaa gcagatgtcc 540  
 tctgcccagg gggctgccct cttgaggaat tctctgtgta tgggaacata gtatatgctt 600  
 ctgtatcgag catatgtggg gctgctgtcc acaggggagt aatcagcaac tcagggggac 660  
 ctgtacgagt ctatagccta cctggtcgag aaaactattc ctcagtagat gccaatggca 720  
 tccagtctca aatgctttct agatggctct cttctttcac agtaactaaa ggcaaaagta 780  
 gtacacagga ggccacagga caagcagtgt ccacagcaca tccaccaaca ggtaaacgac 840  
 taaagaaaac acccgagaag aaaactggca ataaagattg taaagcagac attgcatttc 900  
 tgattgatgg aagctttaat attgggcagc gccgatttaa tttacagaag aattttgttg 960  
 gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtgggc cttgttcaag 1020  
 ccagtgaaca tcccaaaata gaattttact tgaaaaactt tacatcagcc aaagatgttt 1080  
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<210> 227

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&lt;211&gt; 550

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 227

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Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile  
 20 25 30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val  
 35 40 45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn  
 50 55 60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg  
 65 70 75 80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro  
 85 90 95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln  
 100 105 110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser  
 115 120 125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro  
 130 135 140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys  
 145 150 155 160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile  
 165 170 175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala  
 180 185 190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln  
 195 200 205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser  
 210 215 220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly  
 225 230 235 240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe  
 245 250 255

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Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val  
 260 265 270  
 Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val  
 275 280 285  
 Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro  
 290 295 300  
 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320  
 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
 325 330 335  
 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
 340 345 350  
 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
 355 360 365  
 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
 370 375 380  
 Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
 385 390 395 400  
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
 405 410 415  
 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
 420 425 430  
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
 435 440 445  
 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
 450 455 460  
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
 465 470 475 480  
 Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495  
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
 500 505 510  
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
 515 520 525  
 Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp  
 530 535 540

0505348 071301

Phe Leu Glu Ser Gln Gln  
545 550

<210> 228  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 228  
tggtctcgca caccgatc 18

<210> 229  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 229  
ctgctgtcca caggggag 18

<210> 230  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 230  
ccttgaagca tactgctc 18

<210> 231  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 231  
gagatagcaa tttccgcc 18

<210> 232

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FOR 20 34E50650



<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 232  
 ttctctcaaga gggcagcc

18

<210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 233  
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24

<210> 234  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 234  
 gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg

45

<210> 235  
 <211> 2586  
 <212> DNA  
 <213> Homo sapiens

<400> 235  
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 gcctgctgct ggcggcgggc gtccccacgg ccccgcgccc cgctccgacg gcgacctcgg 240  
 ctccagtcaa gcccgggccc gctctcagct acccgcagga ggaggccacc ctcaatgaga 300  
 tggtccgcga gggtgaggaa ctgatggagg acacgcagca caaattgcgc agcgcggtgg 360  
 aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaact 420  
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 acgaggactg tgggcccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660  
 catgcccggg ccagaggatg ctctgcaccc gggacagtga gtgctgtgga gaccagctgt 720

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<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala  
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Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val  
 20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn  
 35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys  
 50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys  
 65 70 75 80

0905343.01301

<210> 237

<211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 237  
 ggagctgcac cccttgc 17

<210> 238  
 <211> 49  
 <212> DNA  
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 <223> Synthetic Oligonucleotide Probe

<400> 238  
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<210> 239  
 <211> 24  
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 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 239  
 gcagagcgga gatgcagcgg ctg 24

<210> 240  
 <211> 18  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 240  
 ttggcagctt catggagg 18

<210> 241  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 241  
 cctgggcaaa aatgcaac 18

<210> 242  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 242  
 ctccagctcc tggcgcacct cctc

24

<210> 243  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Oligonucleotide Probe

<400> 243  
 ggctctcagc taccgcgag gagcgaggcc accctcaatg agatg

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<210> 244  
 <211> 3679  
 <212> DNA  
 <213> Homo Sapien

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 aataaaaata aataataaca ataaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

Met Arg Leu Leu Val Ala Pro Leu Leu Leu Ala Trp Val Ala Gly  
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Ala Thr Ala Thr Val Pro Val Val Pro Trp His Val Pro Cys Pro  
 20 25 30

Pro Gln Cys Ala Cys Gln Ile Arg Pro Trp Tyr Thr Pro Arg Ser  
 35 40 45

Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu  
 50 55 60

Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu  
 65 70 75

Leu Gln Ser Asn Ser Ile Val Arg Val Asp Gln Ser Glu Leu Gly  
 80 85 90

Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe  
 95 100 105

Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu  
 110 115 120

Ser Leu His Leu Glu Glu Asn Gln Leu Thr Arg Leu Glu Asp His  
 125 130 135

Ser Phe Ala Gly Leu Ala Ser Leu Gln Glu Leu Tyr Leu Asn His  
 140 145 150

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Asn	Gln	Leu	Tyr	Arg	Ile	Ala	Pro	Arg	Ala	Phe	Ser	Gly	Leu	Ser	155	160	165
Asn	Leu	Leu	Arg	Leu	His	Leu	Asn	Ser	Asn	Leu	Leu	Arg	Ala	Ile	170	175	180
Asp	Ser	Arg	Trp	Phe	Glu	Met	Leu	Pro	Asn	Leu	Glu	Ile	Leu	Met	185	190	195
Ile	Gly	Gly	Asn	Lys	Val	Asp	Ala	Ile	Leu	Asp	Met	Asn	Phe	Arg	200	205	210
Pro	Leu	Ala	Asn	Leu	Arg	Ser	Leu	Val	Leu	Ala	Gly	Met	Asn	Leu	215	220	225
Arg	Glu	Ile	Ser	Asp	Tyr	Ala	Leu	Glu	Gly	Leu	Gln	Ser	Leu	Glu	230	235	240
Ser	Leu	Ser	Phe	Tyr	Asp	Asn	Gln	Leu	Ala	Arg	Val	Pro	Arg	Arg	245	250	255
Ala	Leu	Glu	Gln	Val	Pro	Gly	Leu	Lys	Phe	Leu	Asp	Leu	Asn	Lys	260	265	270
Asn	Pro	Leu	Gln	Arg	Val	Gly	Pro	Gly	Asp	Phe	Ala	Asn	Met	Leu	275	280	285
His	Leu	Lys	Glu	Leu	Gly	Leu	Asn	Asn	Met	Glu	Glu	Leu	Val	Ser	290	295	300
Ile	Asp	Lys	Phe	Ala	Leu	Val	Asn	Leu	Pro	Glu	Leu	Thr	Lys	Leu	305	310	315
Asp	Ile	Thr	Asn	Asn	Pro	Arg	Leu	Ser	Phe	Ile	His	Pro	Arg	Ala	320	325	330
Phe	His	His	Leu	Pro	Gln	Met	Glu	Thr	Leu	Met	Leu	Asn	Asn	Asn	335	340	345
Ala	Leu	Ser	Ala	Leu	His	Gln	Gln	Thr	Val	Glu	Ser	Leu	Pro	Asn	350	355	360
Leu	Gln	Glu	Val	Gly	Leu	His	Gly	Asn	Pro	Ile	Arg	Cys	Asp	Cys	365	370	375
Val	Ile	Arg	Trp	Ala	Asn	Ala	Thr	Gly	Thr	Arg	Val	Arg	Phe	Ile	380	385	390
Glu	Pro	Gln	Ser	Thr	Leu	Cys	Ala	Glu	Pro	Pro	Asp	Leu	Gln	Arg	395	400	405
Leu	Pro	Val	Arg	Glu	Val	Pro	Phe	Arg	Glu	Met	Thr	Asp	His	Cys			

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	410		415		420
Leu Pro Leu Ile	Ser Pro Arg Ser Phe	Pro Pro Ser Leu Gln Val			
	425		430		435
Ala Ser Gly Glu	Ser Met Val Leu His	Cys Arg Ala Leu Ala Glu			
	440		445		450
Pro Glu Pro Glu	Ile Tyr Trp Val Thr	Pro Ala Gly Leu Arg Leu			
	455		460		465
Thr Pro Ala His	Ala Gly Arg Arg Tyr	Arg Val Tyr Pro Glu Gly			
	470		475		480
Thr Leu Glu Leu	Arg Arg Val Thr Ala	Glu Glu Ala Gly Leu Tyr			
	485		490		495
Thr Cys Val Ala	Gln Asn Leu Val Gly	Ala Asp Thr Lys Thr Val			
	500		505		510
Ser Val Val Val	Gly Arg Ala Leu Leu	Gln Pro Gly Arg Asp Glu			
	515		520		525
Gly Gln Gly Leu	Glu Leu Arg Val Gln	Glu Thr His Pro Tyr His			
	530		535		540
Ile Leu Leu Ser	Trp Val Thr Pro Pro	Asn Thr Val Ser Thr Asn			
	545		550		555
Leu Thr Trp Ser	Ser Ala Ser Ser Leu	Arg Gly Gln Gly Ala Thr			
	560		565		570
Ala Leu Ala Arg	Leu Pro Arg Gly Thr	His Ser Tyr Asn Ile Thr			
	575		580		585
Arg Leu Leu Gln	Ala Thr Glu Tyr Trp	Ala Cys Leu Gln Val Ala			
	590		595		600
Phe Ala Asp Ala	His Thr Gln Leu Ala	Cys Val Trp Ala Arg Thr			
	605		610		615
Lys Glu Ala Thr	Ser Cys His Arg Ala	Leu Gly Asp Arg Pro Gly			
	620		625		630
Leu Ile Ala Ile	Leu Ala Leu Ala Val	Leu Leu Leu Ala Ala Gly			
	635		640		645
Leu Ala Ala His	Leu Gly Thr Gly Gln	Pro Arg Lys Gly Val Gly			
	650		655		660
Gly Arg Arg Pro	Leu Pro Pro Ala Trp	Ala Phe Trp Gly Trp Ser			
	665		670		675

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Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp  
                     680                    685                    690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu  
                     695                    700                    705

Leu Pro Pro Leu Ser Gln Asn Ser  
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<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

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<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgctg atggagacca gctc 24

<210> 248

<211> 45

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

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<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

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 a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

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Cys	Tyr	Thr	Val	Tyr	Tyr	Val	His	Asn	Ile	Lys	Phe	Asp	Val	Asp	20	25	30	
Cys	Thr	Val	Asp	Ile	Glu	Ser	Leu	Thr	Gly	Tyr	Arg	Thr	Tyr	Arg	35	40	45	
Cys	Ala	His	Pro	Leu	Ala	Thr	Leu	Phe	Lys	Ile	Leu	Ala	Ser	Phe	50	55	60	
Tyr	Ile	Ser	Leu	Val	Ile	Phe	Tyr	Gly	Leu	Ile	Cys	Met	Tyr	Thr	65	70	75	
Leu	Trp	Trp	Met	Leu	Arg	Arg	Ser	Leu	Lys	Lys	Tyr	Ser	Phe	Glu	80	85	90	
Ser	Ile	Arg	Glu	Glu	Ser	Ser	Tyr	Ser	Asp	Ile	Pro	Asp	Val	Lys				

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Asn Asp Phe Ala	Phe Met Leu His Leu	Ile Asp Gln Tyr Asp	Pro		
	110		115		120
Leu Tyr Ser Lys	Arg Phe Ala Val Phe	Leu Ser Glu Val Ser	Glu		
	125		130		135
Asn Lys Leu Arg	Gln Leu Asn Leu Asn	Asn Glu Trp Thr Leu	Asp		
	140		145		150
Lys Leu Arg Gln	Arg Leu Thr Lys Asn	Ala Gln Asp Lys Leu	Glu		
	155		160		165
Leu His Leu Phe	Met Leu Ser Gly Ile	Pro Asp Thr Val Phe	Asp		
	170		175		180
Leu Val Glu Leu	Glu Val Leu Lys Leu	Glu Leu Ile Pro Asp	Val		
	185		190		195
Thr Ile Pro Pro	Ser Ile Ala Gln Leu	Thr Gly Leu Lys Glu	Leu		
	200		205		210
Trp Leu Tyr His	Thr Ala Ala Lys Ile	Glu Ala Pro Ala Leu	Ala		
	215		220		225
Phe Leu Arg Glu	Asn Leu Arg Ala Leu	His Ile Lys Phe Thr	Asp		
	230		235		240
Ile Lys Glu Ile	Pro Leu Trp Ile Tyr	Ser Leu Lys Thr Leu	Glu		
	245		250		255
Glu Leu His Leu	Thr Gly Asn Leu Ser	Ala Glu Asn Asn Arg	Tyr		
	260		265		270
Ile Val Ile Asp	Gly Leu Arg Glu Leu	Lys Arg Leu Lys Val	Leu		
	275		280		285
Arg Leu Lys Ser	Asn Leu Ser Lys Leu	Pro Gln Val Val Thr	Asp		
	290		295		300
Val Gly Val His	Leu Gln Lys Leu Ser	Ile Asn Asn Glu Gly	Thr		
	305		310		315
Lys Leu Ile Val	Leu Asn Ser Leu Lys	Lys Met Ala Asn Leu	Thr		
	320		325		330
Glu Leu Glu Leu	Ile Arg Cys Asp Leu	Glu Arg Ile Pro His	Ser		
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Ile Phe Ser Leu	His Asn Leu Gln Glu	Ile Asp Leu Lys Asp	Asn		
	350		355		360

T0E120"84E50660

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His  
 365 370 375  
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 Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu  
 395 400 405  
 Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys  
 410 415 420  
 Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe  
 425 430 435  
 Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala  
 440 445 450  
 Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln  
 455 460 465  
 Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln  
 470 475 480  
 Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile  
 485 490 495  
 Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly  
 500 505 510  
 Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp  
 515 520 525  
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 530 535 540  
 Ala Asp Lys Glu Gln Ala  
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<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 251

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<210> 252

<211> 24

0990548 07301



<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

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 tgggattatg tgacgggtccg caaggatgcc tacatgttct ggtggctcta 200  
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<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

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			20					25					30	
Trp	Pro	Thr	Glu	Glu	Gly	Lys	Glu	Val	Trp	Asp	Tyr	Val	Thr	Val
			35					40					45	

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Arg	Lys	Asp	Ala	Tyr	Met	Phe	Trp	Trp	Leu	Tyr	Tyr	Ala	Thr	Asn	
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Ser	Cys	Lys	Asn	Phe	Ser	Glu	Leu	Pro	Leu	Val	Met	Trp	Leu	Gln	
				65					70					75	
Gly	Gly	Pro	Gly	Gly	Ser	Ser	Thr	Gly	Phe	Gly	Asn	Phe	Glu	Glu	
				80					85					90	
Ile	Gly	Pro	Leu	Asp	Ser	Asp	Leu	Lys	Pro	Arg	Lys	Thr	Thr	Trp	
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Leu	Gln	Ala	Ala	Ser	Leu	Leu	Phe	Val	Asp	Asn	Pro	Val	Gly	Thr	
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Gly	Phe	Ser	Tyr	Val	Asn	Gly	Ser	Gly	Ala	Tyr	Ala	Lys	Asp	Leu	
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Ala	Met	Val	Ala	Ser	Asp	Met	Met	Val	Leu	Leu	Lys	Thr	Phe	Phe	
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Ser	Cys	His	Lys	Glu	Phe	Gln	Thr	Val	Pro	Phe	Tyr	Ile	Phe	Ser	
				155					160					165	
Glu	Ser	Tyr	Gly	Gly	Lys	Met	Ala	Ala	Gly	Ile	Gly	Leu	Glu	Leu	
				170					175					180	
Tyr	Lys	Ala	Ile	Gln	Arg	Gly	Thr	Ile	Lys	Cys	Asn	Phe	Ala	Gly	
				185					190					195	
Val	Ala	Leu	Gly	Asp	Ser	Trp	Ile	Ser	Pro	Val	Asp	Ser	Val	Leu	
				200					205					210	
Ser	Trp	Gly	Pro	Tyr	Leu	Tyr	Ser	Met	Ser	Leu	Leu	Glu	Asp	Lys	
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Gly	Leu	Ala	Glu	Val	Ser	Lys	Val	Ala	Glu	Gln	Val	Leu	Asn	Ala	
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				245					250					255	
Ala	Glu	Met	Ile	Ile	Glu	Gln	Asn	Thr	Asp	Gly	Val	Asn	Phe	Tyr	
				260					265					270	
Asn	Ile	Leu	Thr	Lys	Ser	Thr	Pro	Thr	Ser	Thr	Met	Glu	Ser	Ser	
				275					280					285	
Leu	Glu	Phe	Thr	Gln	Ser	His	Leu	Val	Cys	Leu	Cys	Gln	Arg	His	
				290					295					300	
Val	Arg	His	Leu	Gln	Arg	Asp	Ala	Leu	Ser	Gln	Leu	Met	Asn	Gly	

0905348 "071301  
FOET 20" 84E50660

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Gly Gly Gln Ala Thr Asn Val Phe Val	Asn Met Glu Glu Asp Phe	
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp	Glu Leu Leu Glu Ala Gly	
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln	Leu Asp Leu Ile Val Asp	
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg	Lys Leu Lys Trp Pro Glu	
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp	Lys Ala Leu Tyr Ser Asp	
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe	Val Lys Ser Tyr Lys Asn	
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala	Gly His Met Val Pro Ser	
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Asp Gln Gly Asp Met Ala Leu Lys Met	Met Arg Leu Val Thr Gln	
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Gln Glu

&lt;210&gt; 256

&lt;211&gt; 1100

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 256

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tgctgctggc tcgggctgga ctcaggaagc cggagtcgca ggaggcggcg 100

ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150

tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200

tgtgggattc ccacgtatgc ggagtgcgcc tgctcagcca ccgtggggca 250

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 ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550  
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<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg  
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Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser  
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Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly  
 35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg  
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Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg  
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Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu  
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Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
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 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
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 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
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 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
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 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
 185 190 195  
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
 200 205 210  
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
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 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly  
 230 235 240  
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
 245 250 255  
 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
 260 265 270  
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
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&lt;210&gt; 258

&lt;211&gt; 2427

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 258

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09905348-01301

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<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

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Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

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Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu	35		40		45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg	50		55		60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln	65		70		75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg	80		85		90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala	95		100		105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu	110		115		120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly	125		130		135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val	140		145		150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro	155		160		165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser	170		175		180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly	185		190		195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn	200		205		210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln	215		220		225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu	230		235		240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala	245		250		255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly	260		265		270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala	275		280		285

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Asn	Ile	Ser	Thr	Trp	Val	Tyr	Ser	Ser	Pro	Gly	Arg	His	Glu	Gly	
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Gln	Glu	Pro	Phe	Leu	Gln	Trp	Leu	Met	Leu	Leu	Ser	Asn	Glu	Ser	
				305					310					315	
Ala	Leu	Pro	His	Val	His	Thr	Val	Ser	Tyr	Gly	Asp	Asp	Glu	Asp	
				320					325					330	
Ser	Leu	Ser	Ser	Ala	Tyr	Ile	Gln	Arg	Val	Asn	Thr	Glu	Leu	Met	
				335					340					345	
Lys	Ala	Ala	Ala	Arg	Gly	Leu	Thr	Leu	Leu	Phe	Ala	Ser	Gly	Asp	
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Ser	Gly	Ala	Gly	Cys	Trp	Ser	Val	Ser	Gly	Arg	His	Gln	Phe	Arg	
				365					370					375	
Pro	Thr	Phe	Pro	Ala	Ser	Ser	Pro	Tyr	Val	Thr	Thr	Val	Gly	Gly	
				380					385					390	
Thr	Ser	Phe	Gln	Glu	Pro	Phe	Leu	Ile	Thr	Asn	Glu	Ile	Val	Asp	
				395					400					405	
Tyr	Ile	Ser	Gly	Gly	Gly	Phe	Ser	Asn	Val	Phe	Pro	Arg	Pro	Ser	
				410					415					420	
Tyr	Gln	Glu	Glu	Ala	Val	Thr	Lys	Phe	Leu	Ser	Ser	Ser	Pro	His	
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Leu	Pro	Pro	Ser	Ser	Tyr	Phe	Asn	Ala	Ser	Gly	Arg	Ala	Tyr	Pro	
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Asp	Val	Ala	Ala	Leu	Ser	Asp	Gly	Tyr	Trp	Val	Val	Ser	Asn	Arg	
				455					460					465	
Val	Pro	Ile	Pro	Trp	Val	Ser	Gly	Thr	Ser	Ala	Ser	Thr	Pro	Val	
				470					475					480	
Phe	Gly	Gly	Ile	Leu	Ser	Leu	Ile	Asn	Glu	His	Arg	Ile	Leu	Ser	
				485					490					495	
Gly	Arg	Pro	Pro	Leu	Gly	Phe	Leu	Asn	Pro	Arg	Leu	Tyr	Gln	Gln	
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His	Gly	Ala	Gly	Leu	Phe	Asp	Val	Thr	Arg	Gly	Cys	His	Glu	Ser	
				515					520					525	
Cys	Leu	Asp	Glu	Glu	Val	Glu	Gly	Gln	Gly	Phe	Cys	Ser	Gly	Pro	
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Gly	Trp	Asp	Pro	Val	Thr	Gly	Trp	Gly	Thr	Pro	Thr	Ser	Gln	Leu	
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09905348-071304

Cys

&lt;210&gt; 260

&lt;211&gt; 1638

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 260

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<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Phe	Leu	Leu
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Cys	Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro
				20					25					30

Thr	Trp	Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr
				35					40					45

Leu	Asn	Leu	Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu
				50					55					60

Val	Ser	Ser	Ser	Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu
				65					70					75

Pro	Thr	Tyr	Glu	Glu	Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu
				80					85					90

Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
				95					100					105

Leu	Ser	Ser	Ser	Gly	Asp	Gly	Ala	Gln	His	Arg	Asp	Ser	Gly	Ser
				110					115					120

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Ser Gly Lys Ser	Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser	125	130	135
Arg Phe Ser Ile	Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe	140	145	150
Ser Thr Ser Val	Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val	155	160	165
Ala Glu Lys His	Val Leu Thr Ala Ala His Cys Ile His Asp Gly	170	175	180
Lys Thr Tyr Val	Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu	185	190	195
Lys Pro Lys Phe	Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr	200	205	210
Ser Ala Met Pro	Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys	215	220	225
Arg Thr His Val	Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp	230	235	240
Ile Gly Met Asp	Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro	245	250	255
His Lys Arg Lys	Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys	260	265	270
Gln Leu Pro Gly	Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp	275	280	285
Arg Pro Gly Asn	Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu	290	295	300
Thr Tyr Asp Leu	Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala	305	310	315
Ser Gly Ser Gly	Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln	320	325	330
Lys Trp Glu Arg	Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp	335	340	345
Val Asp Met Asn	Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg	350	355	360
Ile Thr Pro Leu	Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly	365	370	375
Asn Tyr Leu Asp	Cys Arg Glu Gly	380		

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 <211> 1378  
 <212> DNA  
 <213> Homo Sapien

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<210> 263

<211> 317

<212> PRT

<213> Homo Sapien.

<400> 263

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Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln	35	40	45	
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu	50	55	60	
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys	65	70	75	
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	80	85	90	
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu	95	100	105	
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys	110	115	120	
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys	125	130	135	
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser	140	145	150	
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala	155	160	165	
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp	170	175	180	

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Gly	Ser	Ile	Gln	Asp	Gly	Val	Pro	Leu	Pro	His	Pro	Gln	Thr	Leu
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Gln	Lys	Leu	Lys	Val	Pro	Ile	Ile	Asp	Ser	Glu	Val	Cys	Ser	His
				200					205					210
Leu	Tyr	Trp	Arg	Gly	Ala	Gly	Gln	Gly	Pro	Ile	Thr	Glu	Asp	Met
				215					220					225
Leu	Cys	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	Arg	Asp	Ala	Cys	Leu	Gly
				230					235					240
Asp	Ser	Gly	Gly	Pro	Leu	Met	Cys	Gln	Val	Asp	Gly	Ala	Trp	Leu
				245					250					255
Leu	Ala	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Gly	Cys	Ala	Glu	Arg	Asn
				260					265					270
Arg	Pro	Gly	Val	Tyr	Ile	Ser	Leu	Ser	Ala	His	Arg	Ser	Trp	Val
				275					280					285
Glu	Lys	Ile	Val	Gln	Gly	Val	Gln	Leu	Arg	Gly	Arg	Ala	Gln	Gly
				290					295					300
Gly	Gly	Ala	Leu	Arg	Ala	Pro	Ser	Gln	Gly	Ser	Gly	Ala	Ala	Ala
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Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

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<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

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<210> 266

<211> 24

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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 266  
agctctagac caatgccagc ttcc 24

<210> 267  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
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<210> 268  
<211> 25  
<212> DNA  
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<210> 269  
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T0E720"84E50660

<210> 271  
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<212> PRT

<213> Homo Sapien

<400> 285

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Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala	
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Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp	
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Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val	
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Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe	
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Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu	
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Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys	
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Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	
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Glu Pro Pro Gly	Asn Val Lys Gly Lys	Arg Pro Tyr Gln Glu Gly
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Thr Pro Cys Ser	Gln Cys Pro Ser Gly	Tyr His Cys Lys Asn Ser
	185	190 195
Leu Cys Glu Pro	Ile Gly Ser Pro Glu	Asp Ala Gln Asp Leu Pro
	200	205 210
Tyr Leu Val Thr	Glu Ala Pro Ser Phe	Arg Ala Thr Glu Ala Ser
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Asp Ser Arg Lys	Met Gly Thr Pro Ser	Ser Leu Ala Thr Gly Ile
	230	235 240
Pro Ala Phe Leu	Val Thr Glu Val Ser	Gly Ser Leu Ala Thr Lys
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Ala Leu Pro Ala	Val Glu Thr Gln Ala	Pro Thr Ser Leu Ala Thr
	260	265 270
Lys Asp Pro Pro	Ser Met Ala Thr Glu	Ala Pro Pro Cys Val Thr
	275	280 285
Thr Glu Val Pro	Ser Ile Leu Ala Ala	His Ser Leu Pro Ser Leu
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Asp Glu Glu Pro	Val Thr Phe Pro Lys	Ser Thr His Val Pro Ile
	305	310 315
Pro Lys Ser Ala	Asp Lys Val Thr Asp	Lys Thr Lys Val Pro Ser
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Arg Ser Pro Glu	Asn Ser Leu Asp Pro	Lys Met Ser Leu Thr Gly
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	365	370 375
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Gly His Thr Ser	Ser Lys Ser Leu Pro	Asn Phe Pro Asn Thr Ser
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<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

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Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu	35	40	45
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Ala	Leu	Gln	Leu	Lys	Tyr	Leu	Tyr	Leu	Asn	Ser	Asn	Arg	Val	Thr	110	115	120
Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu	125	130	135
Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys	140	145	150
Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn	155	160	165
Lys	Ile	Lys	Asn	Val	Asp	Gly	Leu	Thr	Phe	Gln	Gly	Leu	Gly	Ala	170	175	180
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Asp	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Asn	Met	Glu	Ile	Leu	Gln	Leu	200	205	210
Asp	His	Asn	Asn	Leu	Thr	Glu	Ile	Thr	Lys	Gly	Trp	Leu	Tyr	Gly	215	220	225
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Phe	Leu	Gly	Leu	Ser	Leu	Leu	Asn	Thr	Leu	His	Ile	Gly	Asn	Asn	275	280	285
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0905348-071301

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Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
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Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
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Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
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Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
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Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp		
425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala		
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Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser		
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Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn		
515	520	525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn		
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102720" B4E50660

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Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr	Ser
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Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala	Thr
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Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu	Asp
635	640		645
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile	Ala
650	655		660
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp	Ser
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Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn	Gln
680	685		690
Leu Leu Ile Ile	Val Asp Ser Asp Val	Ser Asp Ala Gly Lys	Tyr
695	700		705
Thr Cys Glu Met	Ser Asn Thr Leu Gly	Thr Glu Arg Gly Asn	Val
710	715		720
Arg Leu Ser Val	Ile Pro Thr Pro Thr	Cys Asp Ser Pro Gln	Met
725	730		735
Thr Ala Pro Ser	Leu Asp Asp Asp Gly	Trp Ala Thr Val Gly	Val
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Val Ile Ile Ala	Val Val Cys Cys Val	Val Gly Thr Ser Leu	Val
755	760		765
Trp Val Val Ile	Ile Tyr His Thr Arg	Arg Arg Asn Glu Asp	Cys
770	775		780
Ser Ile Thr Asn	Thr Asp Glu Thr Asn	Leu Pro Ala Asp Ile	Pro
785	790		795
Ser Tyr Leu Ser	Ser Gln Gly Thr Leu	Ala Asp Arg Gln Asp	Gly
800	805		810

10ET40" 34E50660

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 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 830 835 840  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
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 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
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 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
 875 880 885  
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
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 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
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TOE7'0" 84E50660

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 291

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<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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Leu	Ala	Leu	Gln	Leu	Leu	Val	Val	Ala	Gly	Leu	Val	Arg	Ala	Gln	35	40	45	
Thr	Cys	Pro	Ser	Val	Cys	Ser	Cys	Ser	Asn	Gln	Phe	Ser	Lys	Val	50	55	60	
Ile	Cys	Val	Arg	Lys	Asn	Leu	Arg	Glu	Val	Pro	Asp	Gly	Ile	Ser	65	70	75	
Thr	Asn	Thr	Arg	Leu	Leu	Asn	Leu	His	Glu	Asn	Gln	Ile	Gln	Ile	80	85	90	
Ile	Lys	Val	Asn	Ser	Phe	Lys	His	Leu	Arg	His	Leu	Glu	Ile	Leu	95	100	105	
Gln	Leu	Ser	Arg	Asn	His	Ile	Arg	Thr	Ile	Glu	Ile	Gly	Ala	Phe	110	115	120	
Asn	Gly	Leu	Ala	Asn	Leu	Asn	Thr	Leu	Glu	Leu	Phe	Asp	Asn	Arg	125	130	135	
Leu	Thr	Thr	Ile	Pro	Asn	Gly	Ala	Phe	Val	Tyr	Leu	Ser	Lys	Leu	140	145	150	
Lys	Glu	Leu	Trp	Leu	Arg	Asn	Asn	Pro	Ile	Glu	Ser	Ile	Pro	Ser				

09905348.071301

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Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly	170		175		180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly	185		190		195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg	200		205		210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp	215		220		225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln	230		235		240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile	245		250		255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val	260		265		270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp	275		280		285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His	290		295		300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp	305		310		315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys	320		325		330
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Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro	350		355		360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys	365		370		375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn	380		385		390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val	395		400		405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp	410		415		420

FOET-0-84250660

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<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

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35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys  
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp  
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys  
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

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Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met		
245	250	255
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260	265	270
Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly		
275	280	285
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn		
290	295	300
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu		
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Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser		
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Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn		
335	340	345
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser		
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Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile		
365	370	375
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
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Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
395	400	405
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
410	415	420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
425	430	435
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
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Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
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Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
470	475	480

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Phe Pro Lys Pro	Gln Ile Thr Val Gln	Pro Glu Thr Gln Ser Ala
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Ile Lys Gly Ser	Asn Leu Ser Phe Ile	Cys Ser Ala Ala Ser Ser
515		520 525
Ser Asp Ser Pro	Met Thr Phe Ala Trp	Lys Lys Asp Asn Glu Leu
530		535 540
Leu His Asp Ala	Glu Met Glu Asn Tyr	Ala His Leu Arg Ala Gln
545		550 555
Gly Gly Glu Val	Met Glu Tyr Thr Thr	Ile Leu Arg Leu Arg Glu
560		565 570
Val Glu Phe Ala	Ser Glu Gly Lys Tyr	Gln Cys Val Ile Ser Asn
575		580 585
His Phe Gly Ser	Ser Tyr Ser Val Lys	Ala Lys Leu Thr Val Asn
590		595 600
Met Leu Pro Ser	Phe Thr Lys Thr Pro	Met Asp Leu Thr Ile Arg
605		610 615
Ala Gly Ala Met	Ala Arg Leu Glu Cys	Ala Ala Val Gly His Pro
620		625 630
Ala Pro Gln Ile	Ala Trp Gln Lys Asp	Gly Gly Thr Asp Phe Pro
635		640 645
Ala Ala Arg Glu	Arg Arg Met His Val	Met Pro Glu Asp Asp Val
650		655 660
Phe Phe Ile Val	Asp Val Lys Ile Glu	Asp Ile Gly Val Tyr Ser
665		670 675
Cys Thr Ala Gln	Asn Ser Ala Gly Ser	Ile Ser Ala Asn Ala Thr
680		685 690
Leu Thr Val Leu	Glu Thr Pro Ser Phe	Leu Arg Pro Leu Leu Asp
695		700 705
Arg Thr Val Thr	Lys Gly Glu Thr Ala	Val Leu Gln Cys Ile Ala
710		715 720
Gly Gly Ser Pro	Pro Pro Lys Leu Asn	Trp Thr Lys Asp Asp Ser
725		730 735
Pro Leu Val Val	Thr Glu Arg His Phe	Phe Ala Ala Gly Asn Gln
740		745 750

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Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr	755	760	765
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Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val	800	805	810
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val	815	820	825
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys	830	835	840
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro	845	850	855
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly	860	865	870
Tyr	Val	Ser	Ser	Glu	Ser	Gly	Ser	His	His	Gln	Phe	Val	Thr	Ser	875	880	885
Ser	Gly	Ala	Gly	Phe	Phe	Leu	Pro	Gln	His	Asp	Ser	Ser	Gly	Thr	890	895	900
Cys	His	Ile	Asp	Asn	Ser	Ser	Glu	Ala	Asp	Val	Glu	Ala	Ala	Thr	905	910	915
Asp	Leu	Phe	Leu	Cys	Pro	Phe	Leu	Gly	Ser	Thr	Gly	Pro	Met	Tyr	920	925	930
Leu	Lys	Gly	Asn	Val	Tyr	Gly	Ser	Asp	Pro	Phe	Glu	Thr	Tyr	His	935	940	945
Thr	Gly	Cys	Ser	Pro	Asp	Pro	Arg	Thr	Val	Leu	Met	Asp	His	Tyr	950	955	960
Glu	Pro	Ser	Tyr	Ile	Lys	Lys	Lys	Glu	Cys	Tyr	Pro	Cys	Ser	His	965	970	975
Pro	Ser	Glu	Glu	Ser	Cys	Glu	Arg	Ser	Phe	Ser	Asn	Ile	Ser	Trp	980	985	990
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&lt;400&gt; 295

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Trp	Gly	Trp	Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Val	Cys	50	55	60	
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Leu	Met	Pro	Asp	Gly	Ser	Cys	Ser	Ser	Ala	Leu	Thr	Cys	Ser	Met	125	130	135	
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<213> Homo Sapien

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<213> Homo Sapien

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Asn	Pro	Val	Ser	Glu	Met	Glu	Ser	Asp	Ile	Ile	Met	Pro	Ile	Ile	
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Tyr	Tyr	Gly	Pro	Tyr	Gly	Leu	Gln	Val	Asn	Ser	Asp	Lys	Gly	Leu	
				230					235						240
Lys	Val	Gly	Glu	Val	Phe	Thr	Val	Asp	Leu	Gly	Glu	Ala	Ile	Leu	
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Phe	Asp	Cys	Ser	Ala	Asp	Ser	His	Pro	Pro	Asn	Thr	Tyr	Ser	Trp	
				260					265						270
Ile	Arg	Arg	Thr	Asp	Asn	Thr	Thr	Tyr	Ile	Ile	Lys	His	Gly	Pro	
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Arg	Leu	Glu	Val	Ala	Ser	Glu	Lys	Val	Ala	Gln	Lys	Thr	Met	Asp	
				290					295						300
Tyr	Val	Cys	Cys	Ala	Tyr	Asn	Asn	Ile	Thr	Gly	Arg	Gln	Asp	Glu	
				305					310						315
Thr	His	Phe	Thr	Val	Ile	Ile	Thr	Ser	Val	Gly	Leu	Glu	Lys	Leu	

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Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly		
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu		
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&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 321

gacacctgtca caaagccagt ggtgc 25

&lt;210&gt; 322

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 322

cactgacagg gttcctcacc cagg 24

&lt;210&gt; 323

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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<212> DNA

<213> Homo Sapien

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<211> 280

<212> PRT

<213> Homo Sapien

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35 40 45

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Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp  
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Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly  
80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His  
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Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys  
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Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile  
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Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser  
140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys  
155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser  
170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu  
185 190 195

Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys  
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<212> DNA

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<211> 533

<212> PRT

<213> Homo Sapien

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Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Lys	Glu	Leu	Val	Gln	Ser	Leu	Lys
			35						40					45

Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
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Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
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Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
			80						85					90

Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
			95						100					105

Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
			110						115					120

Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
			125						130					135

Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
			140						145					150

Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
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Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
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Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
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Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Thr	Lys	Ser	Gln	Val	Leu
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485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp  
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<223> Synthetic Oligonucleotide Probe

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<211> 19

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<223> Synthetic Oligonucleotide Probe

<400> 334

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<223> Synthetic Oligonucleotide Probe

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 aactctacca ccgctgccgc ctcagcaacc tggaggggct agggggccgt 2600  
 gccagctgg ctatggctct ctttgagcag gagcaggcca atagcactta 2650  
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<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

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			20						25					30
Val	Ser	Trp	Ile	Gln	Gly	Glu	Gly	Glu	Asp	Pro	Cys	Val	Glu	Ala
			35						40					45
Val	Gly	Glu	Arg	Gly	Gly	Pro	Gln	Asn	Pro	Asp	Ser	Arg	Ala	Arg
			50						55					60
Leu	Asp	Gln	Ser	Asp	Glu	Asp	Phe	Lys	Pro	Arg	Ile	Val	Pro	Tyr
			65						70					75
Tyr	Arg	Asp	Pro	Asn	Lys	Pro	Tyr	Lys	Lys	Val	Leu	Arg	Thr	Arg
			80						85					90
Tyr	Ile	Gln	Thr	Glu	Leu	Gly	Ser	Arg	Glu	Arg	Leu	Leu	Val	Ala

	95		100		105
Val Leu Thr Ser	Arg Ala Thr Leu Ser	Thr Leu Ala Val Ala Val			
	110		115		120
Asn Arg Thr Val	Ala His His Phe Pro Arg	Leu Leu Tyr Phe Thr			
	125		130		135
Gly Gln Arg Gly	Ala Arg Ala Pro Ala Gly	Met Gln Val Val Ser			
	140		145		150
His Gly Asp Glu	Arg Pro Ala Trp Leu Met	Ser Glu Thr Leu Arg			
	155		160		165
His Leu His Thr	His Phe Gly Ala Asp Tyr	Asp Trp Phe Phe Ile			
	170		175		180
Met Gln Asp Asp	Thr Tyr Val Gln Ala Pro	Arg Leu Ala Ala Leu			
	185		190		195
Ala Gly His Leu	Ser Ile Asn Gln Asp Leu	Tyr Leu Gly Arg Ala			
	200		205		210
Glu Glu Phe Ile	Gly Ala Gly Glu Gln Ala	Arg Tyr Cys His Gly			
	215		220		225
Gly Phe Gly Tyr	Leu Leu Ser Arg Ser Leu	Leu Leu Arg Leu Arg			
	230		235		240
Pro His Leu Asp	Gly Cys Arg Gly Asp Ile	Leu Ser Ala Arg Pro			
	245		250		255
Asp Glu Trp Leu	Gly Arg Cys Leu Ile Asp	Ser Leu Gly Val Gly			
	260		265		270
Cys Val Ser Gln	His Gln Gly Gln Gln Tyr	Arg Ser Phe Glu Leu			
	275		280		285
Ala Lys Asn Arg	Asp Pro Glu Lys Glu Gly	Ser Ser Ala Phe Leu			
	290		295		300
Ser Ala Phe Ala	Val His Pro Val Ser Glu	Gly Thr Leu Met Tyr			
	305		310		315
Arg Leu His Lys	Arg Phe Ser Ala Leu Glu	Leu Glu Arg Ala Tyr			
	320		325		330
Ser Glu Ile Glu	Gln Leu Gln Ala Gln Ile	Arg Asn Leu Thr Val			
	335		340		345
Leu Thr Pro Glu	Gly Glu Ala Gly Leu Ser	Trp Pro Val Gly Leu			
	350		355		360

09905348-071301



Pro	Ala	Pro	Phe	Thr	Pro	His	Ser	Arg	Phe	Glu	Val	Leu	Gly	Trp	365	370	375
Asp	Tyr	Phe	Thr	Glu	Gln	His	Thr	Phe	Ser	Cys	Ala	Asp	Gly	Ala	380	385	390
Pro	Lys	Cys	Pro	Leu	Gln	Gly	Ala	Ser	Arg	Ala	Asp	Val	Gly	Asp	395	400	405
Ala	Leu	Glu	Thr	Ala	Leu	Glu	Gln	Leu	Asn	Arg	Arg	Tyr	Gln	Pro	410	415	420
Arg	Leu	Arg	Phe	Gln	Lys	Gln	Arg	Leu	Leu	Asn	Gly	Tyr	Arg	Arg	425	430	435
Phe	Asp	Pro	Ala	Arg	Gly	Met	Glu	Tyr	Thr	Leu	Asp	Leu	Leu	Leu	440	445	450
Glu	Cys	Val	Thr	Gln	Arg	Gly	His	Arg	Arg	Ala	Leu	Ala	Arg	Arg	455	460	465
Val	Ser	Leu	Leu	Arg	Pro	Leu	Ser	Arg	Val	Glu	Ile	Leu	Pro	Met	470	475	480
Pro	Tyr	Val	Thr	Glu	Ala	Thr	Arg	Val	Gln	Leu	Val	Leu	Pro	Leu	485	490	495
Leu	Val	Ala	Glu	Ala	Ala	Ala	Ala	Pro	Ala	Phe	Leu	Glu	Ala	Phe	500	505	510
Ala	Ala	Asn	Val	Leu	Glu	Pro	Arg	Glu	His	Ala	Leu	Leu	Thr	Leu	515	520	525
Leu	Leu	Val	Tyr	Gly	Pro	Arg	Glu	Gly	Gly	Arg	Gly	Ala	Pro	Asp	530	535	540
Pro	Phe	Leu	Gly	Val	Lys	Ala	Ala	Ala	Ala	Glu	Leu	Glu	Arg	Arg	545	550	555
Tyr	Pro	Gly	Thr	Arg	Leu	Ala	Trp	Leu	Ala	Val	Arg	Ala	Glu	Ala	560	565	570
Pro	Ser	Gln	Val	Arg	Leu	Met	Asp	Val	Val	Ser	Lys	Lys	His	Pro	575	580	585
Val	Asp	Thr	Leu	Phe	Phe	Leu	Thr	Thr	Val	Trp	Thr	Arg	Pro	Gly	590	595	600
Pro	Glu	Val	Leu	Asn	Arg	Cys	Arg	Met	Asn	Ala	Ile	Ser	Gly	Trp	605	610	615
Gln	Ala	Phe	Phe	Pro	Val	His	Phe	Gln	Glu	Phe	Asn	Pro	Ala	Leu	620	625	630

TOCT'0"84E90660

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
 635 640 645  
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
 740 745 750  
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
 755 760 765  
 Gln Glu Gln Ala Asn Ser Thr  
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&lt;210&gt; 340

&lt;211&gt; 1572

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 340

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 ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150  
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccacatgag 200  
 catcatcacc tacaagctcc taacaaagaa gatattcttga aaatttcaga 250  
 ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300  
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 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

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 100120-84E0660

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 aagcttaciaa atacgccttt gataagtata gagaccaata caactgggtc 500  
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 tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600  
 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650  
 gtagaatcaa tgaagagact taacagcctt ctcaatatcc cagaaaagtg 700  
 tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750  
 cagtttgccct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800  
 gatggaaaag atgtatttaa taccaaatct gttgggcttt ctattaaaga 850  
 ggcaatgact tatcacccca accaggtagt agaaggctgt tgttcagata 900  
 tggtgtttac ttttaatgga ctgactccaa atcagatgca tgtgatgatg 950  
 tatgggggtat accgccttag ggcatttggg catattttca atgatgcatt 1000  
 gggtttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050  
 agcgtgaata tgatctttgt ataggacgtg tggtgtcatt atttgtagta 1100  
 gtaactacat atccaatata gctgtatggt tctttttctt ttctaatttg 1150  
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 ggggtggtttt tttctttaaa acacatgaac attgtaaatg tggtggaaaag 1250  
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 tttgctgatt gggttaaaaaa ttttaacagg tcttttagcgt tctaagatat 1400  
 gcaaatgata tctctagttg tgaatttggt attaaagtaa aacttttagc 1450  
 tgtgtgttcc ctttacttct aatactgatt tatgttctaa gcctcccaa 1500  
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<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

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&lt;400&gt; 341

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Ser	Ile	Phe	Cys	Ala	Leu	Ile	Thr	Met	Leu	Gly	His	Ile	Arg	Ile
				20					25					30
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
				35					40					45
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
				50					55					60
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
				65					70					75
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
				80					85					90
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
				95					100					105
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
				110					115					120
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
				125					130					135
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
				140					145					150
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
				155					160					165
Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	Asp	Leu	Glu	Tyr
				170					175					180
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
				185					190					195
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
				200					205					210
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
				215					220					225
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
				230					235					240
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
				245					250					255
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TOET 20-84E50660

Asp Asn Asp

<211> 23

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

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<211> 18

<213> Artificial Sequence

<223> Synthetic Oligonucleotide Probe

ctgggttcttc cttgcacg 18

<211> 28

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<223> Synthetic Oligonucleotide Probe

gcccaaatgc cctaaggcgg tatacccc 28

<211> 50

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 345

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<210> 346

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 346

gggatgcagg tgggtgtctca tgggg 25

<210> 347

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347

ccctcatgta ccggtcc 18

<210> 348

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

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<400> 348

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<210> 349

<211> 47

<212> DNA

<213> Artificial Sequence

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<400> 349

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<210> 350

<211> 48

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TOE"Q" BHE50660

<220>  
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<210> 351  
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<210> 353  
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<220>  
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<210> 354  
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 <210> 356  
 <211> 46  
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 <400> 356  
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 <210> 357  
 <211> 48  
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 <400> 357  
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 <210> 358  
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 <220>  
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 <400> 358  
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 <210> 359  
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090548-01301  
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<210> 360  
<211> 48  
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<210> 361  
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<400> 364

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<210> 365

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<212> DNA

<213> Artificial Sequence

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<400> 365

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<211> 48

<212> DNA

<213> Artificial Sequence

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<210> 367

<211> 47

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

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<211> 48

<212> DNA

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<223> Synthetic Oligonucleotide Probe

<400> 369

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<211> 48

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<400> 370

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<210> 371

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<223> Synthetic Oligonucleotide Probe

<400> 371

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<210> 372

<211> 47

<212> DNA

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<210> 373

<211> 48

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<400> 373

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<210> 374

<211> 47

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TOE1.0" BHE50660

<220>

<223> Synthetic Oligonucleotide Probe

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<210> 375

<211> 48

<212> DNA

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<220>

<223> Synthetic Oligonucleotide Probe

<400> 375

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<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

<400> 376

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 agggagggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100  
 aaaaaatgaa ttcattctaaa tcatctgaaa cacaatgcac agagagagga 150  
 tgcttctctt cccaaatggt cttatggact gttgctggga tccccatcct 200  
 atttctcagt gcctgtttca tcaccagatg tgttgtagaca tttcgcatct 250  
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 ctctctgct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350  
 gaactgggaa tattttcaat ccagctgcta cttcttttct actgacacca 400  
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<210> 377
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<212> PRT
<213> Homo Sapien
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				20					25					30
Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr
				35					40					45
Phe	Arg	Ile	Phe	Gln	Thr	Cys	Asp	Glu	Lys	Lys	Phe	Gln	Leu	Pro
				50					55					60
Glu	Asn	Phe	Thr	Glu	Leu	Ser	Cys	Tyr	Asn	Tyr	Gly	Ser	Gly	Ser
				65					70					75
Val	Lys	Asn	Cys	Cys	Pro	Leu	Asn	Trp	Glu	Tyr	Phe	Gln	Ser	Ser
				80					85					90
Cys	Tyr	Phe	Phe	Ser	Thr	Asp	Thr	Ile	Ser	Trp	Ala	Leu	Ser	Leu
				95					100					105
Lys	Asn	Cys	Ser	Ala	Met	Gly	Ala	His	Leu	Val	Val	Ile	Asn	Ser
				110					115					120
Gln	Glu	Glu	Gln	Glu	Phe	Leu	Ser	Tyr	Lys	Lys	Pro	Lys	Met	Arg
				125					130					135
Glu	Phe	Phe	Ile	Gly	Leu	Ser	Asp	Gln	Val	Val	Glu	Gly	Gln	Trp
				140					145					150
Gln	Trp	Val	Asp	Gly	Thr	Pro	Leu	Thr	Lys	Ser	Leu	Ser	Phe	Trp
				155					160					165
Asp	Val	Gly	Glu	Pro	Asn	Asn	Ile	Ala	Thr	Leu	Glu	Asp	Cys	Ala
				170					175					180

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
 185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile  
 200 205 210

Asn Pro Leu Asn Lys Gly Lys Ser Leu  
 215

<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

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Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg	110	115	120	
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